



#3

SEQUENCE LISTING

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<120> Monoterpene Synthases from Grand Fir (Abies Grandis)

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<140> 10/025,145

<141> 2001-12-19

<150> US 09/360,545

<151> 1999-07-26

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<151> 1998-07-10

<150> US 60/052,249

<151> 1997-07-11

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<170> PatentIn version 3.1

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 Asp Glu Ile Lys Ser Ala Leu Asp Tyr Val Tyr Ser Tyr Trp Gly Glu

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Val Ser Ser Leu Ser Arg Glu Ile Gly Asp Val Leu Glu Tyr Gly Trp
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Met Lys Asp Asn Pro Gly Val Ser Glu Glu Asp Ala Leu Asp His Ile
545 550 555 560

Asn Ala Met Ile Ser Asp Val Ile Lys Gly Leu Asn Trp Glu Leu Leu
565 570 575

Lys Pro Asp Ile Asn Val Pro Ile Ser Ala Lys Lys His Ala Phe Asp
580 585 590

Ile Ala Arg Ala Phe His Tyr Gly Tyr Lys Tyr Arg Asp Gly Tyr Ser
595 600 605

Val Ala Asn Val Glu Thr Lys Ser Leu Val Thr Arg Thr Leu Leu Glu
610 615 620

Ser Val Pro Leu
625

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<212> DNA
<213> Abies Grandis

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<222> (73)..(1986)
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aggcaggaat cc atg gct ctc ctt tct atc gta tct ttg cag gtt ccc aaa 111
Met Ala Leu Leu Ser Ile Val Ser Leu Gln Val Pro Lys
1 5 10

tcc tgc ggg ctg aaa tcg ttg atc agt tcc agc aat gtg cag aag gct 159
Ser Cys Gly Leu Lys Ser Leu Ile Ser Ser Ser Asn Val Gln Lys Ala
15 20 25

ctc tgt atc tct aca gca gtc cca aca ctc aga atg cgt agg cga cag 207
Leu Cys Ile Ser Thr Ala Val Pro Thr Leu Arg Met Arg Arg Arg Gln
30 35 40 45

aaa gct ctg gtc atc aac atg aaa ttg acc act gta tcc cat cgt gat 255
Lys Ala Leu Val Ile Asn Met Lys Leu Thr Thr Val Ser His Arg Asp
50 55 60

gat aat ggt ggt ggt gta ctg caa aga cgc ata gcc gat cat cat ccc 303
Asp Asn Gly Gly Gly Val Leu Gln Arg Arg Ile Ala Asp His His Pro
65 70 75

aac ctg tgg gaa gat gat ttc ata caa tca ttg tcc tca cct tat ggg 351
Asn Leu Trp Glu Asp Asp Phe Ile Gln Ser Leu Ser Ser Pro Tyr Gly
80 85 90

gga tct tcg tac agt gaa cgt gct gag aca gtc gtt gag gaa gta aaa 399
Gly Ser Ser Tyr Ser Glu Arg Ala Glu Thr Val Val Glu Glu Val Lys
95 100 105

gag atg ttc aat tca ata cca aat aat aga gaa tta ttt ggt tcc caa 447
Glu Met Phe Asn Ser Ile Pro Asn Asn Arg Glu Leu Phe Gly Ser Gln
110 115 120 125

aat gat ctc ctt aca cgc ctt tgg atg gtg gat agc att gaa cgt ctg 495
Asn Asp Leu Leu Thr Arg Leu Trp Met Val Asp Ser Ile Glu Arg Leu
130 135 140

ggg ata gat aga cat ttc caa aat gag ata aga gta gcc ctc gat tat 543
Gly Ile Asp Arg His Phe Gln Asn Glu Ile Arg Val Ala Leu Asp Tyr
145 150 155

gtt tac agt tat tgg aag gaa aag gaa ggc att ggg tgt ggc aga gat 591
Val Tyr Ser Tyr Trp Lys Glu Lys Glu Gly Ile Gly Cys Gly Arg Asp
160 165 170

tct act ttt cct gat ctc aac tcg act gcc ttg gcg ctt cga act ctt 639
Ser Thr Phe Pro Asp Leu Asn Ser Thr Ala Leu Ala Leu Arg Thr Leu
175 180 185

cga ctg cac gga tac aat gtg tct tca gat gtg ctg gaa tac ttc aaa 687
Arg Leu His Gly Tyr Asn Val Ser Ser Asp Val Leu Glu Tyr Phe Lys
190 195 200 205

gat gaa aag ggg cat ttt gcc tgc cct gca atc cta acc gag gga cag 735
Asp Glu Lys Gly His Phe Ala Cys Pro Ala Ile Leu Thr Glu Gly Gln
210 215 220

atc act aga agt gtt cta aat tta tat cgg gct tcc ctg gtc gcc ttt 783
Ile Thr Arg Ser Val Leu Asn Leu Tyr Arg Ala Ser Leu Val Ala Phe

225	230	235	
ccc ggg gag aaa gtt atg gaa gag gct gaa atc ttc tcg gca tct tat Pro Gly Glu Lys Val Met Glu Glu Ala Glu Ile Phe Ser Ala Ser Tyr 240 245 250			831
ttg aaa aaa gtc tta caa aag att ccg gtc tcc aat ctt tca gga gag Leu Lys Lys Val Leu Gln Lys Ile Pro Val Ser Asn Leu Ser Gly Glu 255 260 265			879
ata gaa tat gtt ttg gaa tat ggt tgg cac acg aat ttg ccg aga ttg Ile Glu Tyr Val Leu Glu Tyr Gly Trp His Thr Asn Leu Pro Arg Leu 270 275 280 285			927
gaa gca aga aat tat atc gag gtc tac gag cag agc ggc tat gaa agc Glu Ala Arg Asn Tyr Ile Glu Val Tyr Glu Gln Ser Gly Tyr Glu Ser 290 295 300			975
tta aac gag atg cca tat atg aac atg aag aag ctt tta caa ctt gca Leu Asn Glu Met Pro Tyr Met Asn Met Lys Lys Leu Leu Gln Leu Ala 305 310 315			1023
aaa ttg gag ttc aat atc ttt cac tct ttg caa cta aga gag tta caa Lys Leu Glu Phe Asn Ile Phe His Ser Leu Gln Leu Arg Glu Leu Gln 320 325 330			1071
tct atc tcc aga tgg tgg aaa gaa tca ggt tcg tct caa ctg act ttt Ser Ile Ser Arg Trp Trp Lys Glu Ser Gly Ser Ser Gln Leu Thr Phe 335 340 345			1119
aca cgg cat cgt cac gtg gaa tac tac act atg gca tct tgc att tct Thr Arg His Arg His Val Glu Tyr Tyr Thr Met Ala Ser Cys Ile Ser 350 355 360 365			1167
atg ttg cca aaa cat tca gct ttc aga atg gag ttt gtc aaa gtg tgt Met Leu Pro Lys His Ser Ala Phe Arg Met Glu Phe Val Lys Val Cys 370 375 380			1215
cat ctt gta aca gtt ctc gat gat ata tat gac act ttt gga aca atg His Leu Val Thr Val Leu Asp Asp Ile Tyr Asp Thr Phe Gly Thr Met 385 390 395			1263
aac gaa ctc caa ctt ttt acg gat gca att aag aga tgg gat ttg tca Asn Glu Leu Gln Leu Phe Thr Asp Ala Ile Lys Arg Trp Asp Leu Ser 400 405 410			1311
acg aca agg tgg ctt cca gaa tat atg aaa gga gtg tac atg gac ttg Thr Thr Arg Trp Leu Pro Glu Tyr Met Lys Gly Val Tyr Met Asp Leu 415 420 425			1359
tat caa tgc att aat gaa atg gtg gaa gag gct gag aag act caa ggc Tyr Gln Cys Ile Asn Glu Met Val Glu Glu Ala Glu Lys Thr Gln Gly 430 435 440 445			1407
cga gat atg ctc aac tat att caa aat gct tgg gaa gcc cta ttt gat Arg Asp Met Leu Asn Tyr Ile Gln Asn Ala Trp Glu Ala Leu Phe Asp 450 455 460			1455
acc ttt atg caa gaa gca aag tgg atc tcc agc agt tat ctc cca acg Thr Phe Met Gln Glu Ala Lys Trp Ile Ser Ser Ser Tyr Leu Pro Thr 465 470 475			1503

ttt gag gag tac ttg aag aat gca aaa gtt agt tct ggt tct cgc ata	1551
Phe Glu Glu Tyr Leu Lys Asn Ala Lys Val Ser Ser Gly Ser Arg Ile	
480 485 490	

gcc aca tta caa ccc att ctc act ttg gat gta cca ctt cct gat tac	1599
Ala Thr Leu Gln Pro Ile Leu Thr Leu Asp Val Pro Leu Pro Asp Tyr	
495 500 505	

ata ctg caa gaa att gat tat cca tcc aga ttc aat gag tta gct tcg	1647
Ile Leu Gln Glu Ile Asp Tyr Pro Ser Arg Phe Asn Glu Leu Ala Ser	
510 515 520 525	

tcc atc ctt cga cta cga ggt gac acg cgc tgc tac aag gcg gat agg	1695
Ser Ile Leu Arg Leu Arg Gly Asp Thr Arg Cys Tyr Lys Ala Asp Arg	
530 535 540	

gcc cgt gga gaa gaa gct tca gct ata tcg tgt tat atg aaa gac cat	1743
Ala Arg Gly Glu Glu Ala Ser Ala Ile Ser Cys Tyr Met Lys Asp His	
545 550 555	

cct gga tca ata gag gaa gat gct ctc aat cat atc aac gcc atg atc	1791
Pro Gly Ser Ile Glu Glu Asp Ala Leu Asn His Ile Asn Ala Met Ile	
560 565 570	

agt gat gca atc aga gaa tta aat tgg gag ctt ctc aga ccg gat agc	1839
Ser Asp Ala Ile Arg Glu Leu Asn Trp Glu Leu Leu Arg Pro Asp Ser	
575 580 585	

aaa agt ccc atc tct tcc aag aaa cat gct ttt gac atc acc aga gct	1887
Lys Ser Pro Ile Ser Ser Lys Lys His Ala Phe Asp Ile Thr Arg Ala	
590 595 600 605	

ttc cat cat gtc tac aaa tat cga gat ggt tac act gtt tcc aac aac	1935
Phe His His Val Tyr Lys Tyr Arg Asp Gly Tyr Thr Val Ser Asn Asn	
610 615 620	

gaa aca aag aat ttg gtg atg aaa acc gtt ctt gaa cct ctc gct ttg	1983
Glu Thr Lys Asn Leu Val Met Lys Thr Val Leu Glu Pro Leu Ala Leu	
625 630 635	

taa aaacatatag aatgcattaa aatgtgggaa gtctataatc tagactattc	2036
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tctatctttc ataatgtaga tctggatgtg tattgaactc taataaaaaaa aaa	2089
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 <212> PRT
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<400> 6

Met Ala Leu Leu Ser Ile Val Ser Leu Gln Val Pro Lys Ser Cys Gly
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Leu Lys Ser Leu Ile Ser Ser Ser Asn Val Gln Lys Ala Leu Cys Ile
20 25 30

Ser Thr Ala Val Pro Thr Leu Arg Met Arg Arg Arg Gln Lys Ala Leu
35 40 45

Val Ile Asn Met Lys Leu Thr Thr Val Ser His Arg Asp Asp Asn Gly
50 55 60

Gly Gly Val Leu Gln Arg Arg Ile Ala Asp His His Pro Asn Leu Trp
65 70 75 80

Glu Asp Asp Phe Ile Gln Ser Leu Ser Ser Pro Tyr Gly Gly Ser Ser
85 90 95

Tyr Ser Glu Arg Ala Glu Thr Val Val Glu Glu Val Lys Glu Met Phe
100 105 110

Asn Ser Ile Pro Asn Asn Arg Glu Leu Phe Gly Ser Gln Asn Asp Leu
115 120 125

Leu Thr Arg Leu Trp Met Val Asp Ser Ile Glu Arg Leu Gly Ile Asp
130 135 140

Arg His Phe Gln Asn Glu Ile Arg Val Ala Leu Asp Tyr Val Tyr Ser
145 150 155 160

Tyr Trp Lys Glu Lys Glu Gly Ile Gly Cys Gly Arg Asp Ser Thr Phe
165 170 175

Pro Asp Leu Asn Ser Thr Ala Leu Ala Leu Arg Thr Leu Arg Leu His
180 185 190

Gly Tyr Asn Val Ser Ser Asp Val Leu Glu Tyr Phe Lys Asp Glu Lys
195 200 205

Gly His Phe Ala Cys Pro Ala Ile Leu Thr Glu Gly Gln Ile Thr Arg
210 215 220

Ser Val Leu Asn Leu Tyr Arg Ala Ser Leu Val Ala Phe Pro Gly Glu
225 230 235 240

Lys Val Met Glu Glu Ala Glu Ile Phe Ser Ala Ser Tyr Leu Lys Lys
245 250 255

Val Leu Gln Lys Ile Pro Val Ser Asn Leu Ser Gly Glu Ile Glu Tyr
260 265 270

Val Leu Glu Tyr Gly Trp His Thr Asn Leu Pro Arg Leu Glu Ala Arg

275

280

285

Asn Tyr Ile Glu Val Tyr Glu Gln Ser Gly Tyr Glu Ser Leu Asn Glu
290 295 300

Met Pro Tyr Met Asn Met Lys Lys Leu Leu Gln Leu Ala Lys Leu Glu
305 310 315 320

Phe Asn Ile Phe His Ser Leu Gln Leu Arg Glu Leu Gln Ser Ile Ser
325 330 335

Arg Trp Trp Lys Glu Ser Gly Ser Ser Gln Leu Thr Phe Thr Arg His
340 345 350

Arg His Val Glu Tyr Tyr Thr Met Ala Ser Cys Ile Ser Met Leu Pro
355 360 365

Lys His Ser Ala Phe Arg Met Glu Phe Val Lys Val Cys His Leu Val
370 375 380

Thr Val Leu Asp Asp Ile Tyr Asp Thr Phe Gly Thr Met Asn Glu Leu
385 390 395 400

Gln Leu Phe Thr Asp Ala Ile Lys Arg Trp Asp Leu Ser Thr Thr Arg
405 410 415

Trp Leu Pro Glu Tyr Met Lys Gly Val Tyr Met Asp Leu Tyr Gln Cys
420 425 430

Ile Asn Glu Met Val Glu Glu Ala Glu Lys Thr Gln Gly Arg Asp Met
435 440 445

Leu Asn Tyr Ile Gln Asn Ala Trp Glu Ala Leu Phe Asp Thr Phe Met
450 455 460

Gln Glu Ala Lys Trp Ile Ser Ser Ser Tyr Leu Pro Thr Phe Glu Glu
465 470 475 480

Tyr Leu Lys Asn Ala Lys Val Ser Ser Gly Ser Arg Ile Ala Thr Leu
485 490 495

Gln Pro Ile Leu Thr Leu Asp Val Pro Leu Pro Asp Tyr Ile Leu Gln
500 505 510

Glu Ile Asp Tyr Pro Ser Arg Phe Asn Glu Leu Ala Ser Ser Ile Leu
515 520 525

Arg Leu Arg Gly Asp Thr Arg Cys Tyr Lys Ala Asp Arg Ala Arg Gly
530 535 540

Glu Glu Ala Ser Ala Ile Ser Cys Tyr Met Lys Asp His Pro Gly Ser
545 550 555 560

Ile Glu Glu Asp Ala Leu Asn His Ile Asn Ala Met Ile Ser Asp Ala
565 570 575

Ile Arg Glu Leu Asn Trp Glu Leu Leu Arg Pro Asp Ser Lys Ser Pro
580 585 590

Ile Ser Ser Lys Lys His Ala Phe Asp Ile Thr Arg Ala Phe His His
595 600 605

Val Tyr Lys Tyr Arg Asp Gly Tyr Thr Val Ser Asn Asn Glu Thr Lys
610 615 620

Asn Leu Val Met Lys Thr Val Leu Glu Pro Leu Ala Leu
625 630 635

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<211> 25
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<220>
<223> Degenerate oligonucleotide PCR primer A

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<223> Wherein N=inosine

<400> 7
arraygarra nggnrartay aarga

25

<210> 8
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<212> DNA
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<220>
<223> Degenerate oligonucleotide PCR primer B

<220>
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<222> (1)..(20)
<223> Wherein N=inosine residue

<400> 8
atgytn Cary tntaygargc

20

<210> 9
<211> 24
<212> DNA
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<220>
<223> Degenerate oligonucleotide PCR primer C

<220>
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<222> (1)..(24)
<223> Wherein N=inosine residue

<400> 9
ctnkynrang gncratrta ckt y

24

<210> 10
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Degenerate oligonucleotide PCR primer D

<220>
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<222> (1)..(23)
<223> Wherein N=isonine

<400> 10
gaygaynnnt wygaygcnya ygg

23

<210> 11
<211> 108
<212> DNA
<213> Abies Grandis

<400> 11
gatgatgggt ttgatgcgca cggaacccta gatgaattga agctattcac tgaggctgtg 60
agaagatggg acctctcctt tacagacaac ttccccgatt acatgaaa 108

<210> 12
<211> 104
<212> DNA
<213> Abies Grandis

<400> 12
gacgacgggt atgatgcgca tggaacgatt gacgagcttg aactcttcac atctgcaatt 60
aagagatgga attcatcaga gatagacagc ttccccgact atat 104

<210> 13
<211> 105
<212> DNA
<213> Abies Grandis

<220>
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<222> (1)..(105)
<223> Wherein N=A, C, G or T

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gatgatgggt atgatgcgta cggaacgttg gaagaaatca aaatcatgac agaggggagtg 60
agacgatggg atcttttcggt gaccgcttnc cccgactata tgaaa 105

<210> 14
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<212> DNA
<213> Abies Grandis

<220>
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<222> (1)..(117)
<223> Wherein N=A, C, G or T

<400> 14
gacgatgggt atgatgcgca tggaaccttg gaccaactca aaatctttac agaggggagtg 60
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<210> 15
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<212> DNA
<213> Abies Grandis

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<222> (2)..(2350)
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Gly Tyr Asp Leu Val His Ser Leu Lys Ser Pro Tyr Ile Asp Ser Ser
1 5 10 15

tac aga gaa cgc gcg gag gtc ctt gtt agc gag att aaa gtg atg ctt 97
Tyr Arg Glu Arg Ala Glu Val Leu Val Ser Glu Ile Lys Val Met Leu
20 25 30

aat cca gct att aca gga gat gga gaa tca atg att act cca tct gct 145
Asn Pro Ala Ile Thr Gly Asp Gly Glu Ser Met Ile Thr Pro Ser Ala
35 40 45

tat gac aca gca tgg gta gcg agg gtg ccc gcc att gat ggc tct gct 193

Tyr	Asp	Thr	Ala	Trp	Val	Ala	Arg	Val	Pro	Ala	Ile	Asp	Gly	Ser	Ala		
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cgc	ccg	caa	ttt	ccc	caa	aca	gtt	gac	tgg	att	ttg	aaa	aac	cag	tta	241	
Arg	Pro	Gln	Phe	Pro	Gln	Thr	Val	Asp	Trp	Ile	Leu	Lys	Asn	Gln	Leu	80	
65					70					75							
aaa	gat	ggt	tca	tgg	gga	att	cag	tcc	cac	ttt	ctg	ctg	tcc	gac	cgt	289	
Lys	Asp	Gly	Ser	Trp	Gly	Ile	Gln	Ser	His	Phe	Leu	Leu	Ser	Asp	Arg	95	
				85					90								
ctt	ctt	gcc	act	ctt	tct	tgt	gtt	ctt	gtg	ctc	ctt	aaa	tgg	aac	gtt	337	
Leu	Leu	Ala	Thr	Leu	Ser	Cys	Val	Leu	Val	Leu	Leu	Lys	Trp	Asn	Val	110	
			100					105									
ggg	gat	ctg	caa	gta	gag	cag	gga	att	gaa	ttc	ata	aag	agc	aat	ctg	385	
Gly	Asp	Leu	Gln	Val	Glu	Gln	Gly	Ile	Glu	Phe	Ile	Lys	Ser	Asn	Leu	125	
		115					120										
gaa	cta	gta	aag	gat	gaa	acc	gat	caa	gat	agc	ttg	gta	aca	gac	ttt	433	
Glu	Leu	Val	Lys	Asp	Glu	Thr	Asp	Gln	Asp	Ser	Leu	Val	Thr	Asp	Phe	140	
	130						135										
gag	atc	ata	ttt	cct	tct	ctg	tta	aga	gaa	gct	caa	tct	ctg	cgc	ctc	481	
Glu	Ile	Ile	Phe	Pro	Ser	Leu	Leu	Arg	Glu	Ala	Gln	Ser	Leu	Arg	Leu	160	
145					150					155							
gga	ctt	ccc	tac	gac	ctg	cct	tat	ata	cat	ctg	ttg	cag	act	aaa	cgg	529	
Gly	Leu	Pro	Tyr	Asp	Leu	Pro	Tyr	Ile	His	Leu	Leu	Gln	Thr	Lys	Arg	175	
				165					170								
cag	gaa	aga	tta	gca	aaa	ctt	tca	agg	gag	gaa	att	tat	gcg	gtt	ccg	577	
Gln	Glu	Arg	Leu	Ala	Lys	Leu	Ser	Arg	Glu	Glu	Ile	Tyr	Ala	Val	Pro	190	
			180					185									
tcg	cca	ttg	ttg	tat	tct	tta	gag	gga	ata	caa	gat	ata	gtt	gaa	tgg	625	
Ser	Pro	Leu	Leu	Tyr	Ser	Leu	Glu	Gly	Ile	Gln	Asp	Ile	Val	Glu	Trp	205	
		195					200										
gaa	cga	ata	atg	gaa	gtt	caa	agt	cag	gat	ggg	tct	ttc	tta	agc	tca	673	
Glu	Arg	Ile	Met	Glu	Val	Gln	Ser	Gln	Asp	Gly	Ser	Phe	Leu	Ser	Ser	220	
	210					215											
cct	gct	tct	act	gcc	tgc	gtt	ttc	atg	cac	aca	gga	gac	gcg	aaa	tgc	721	
Pro	Ala	Ser	Thr	Ala	Cys	Val	Phe	Met	His	Thr	Gly	Asp	Ala	Lys	Cys	240	
225					230					235							
ctt	gaa	ttc	ttg	aac	agt	gtg	atg	atc	aag	ttt	gga	aat	ttt	gtt	ccc	769	
Leu	Glu	Phe	Leu	Asn	Ser	Val	Met	Ile	Lys	Phe	Gly	Asn	Phe	Val	Pro	255	
				245					250								
tgc	ctg	tat	cct	gtg	gat	ctg	ctg	gaa	cgc	ctg	ttg	atc	gta	gat	aat	817	
Cys	Leu	Tyr	Pro	Val	Asp	Leu	Leu	Glu	Arg	Leu	Leu	Ile	Val	Asp	Asn	270	
			260					265									
att	gta	cgc	ctt	gga	atc	tat	aga	cac	ttt	gaa	aag	gaa	atc	aag	gaa	865	
Ile	Val	Arg	Leu	Gly	Ile	Tyr	Arg	His	Phe	Glu	Lys	Glu	Ile	Lys	Glu	285	
		275					280										
gct	ctt	gat	tat	gtt	tac	agg	cat	tgg	aac	gaa	aga	gga	att	ggg	tgg	913	
Ala	Leu	Asp	Tyr	Val	Tyr	Arg	His	Trp	Asn	Glu	Arg	Gly	Ile	Gly	Trp		

290	295	300	
ggc aga cta aat ccc ata gca gat ctt gag acc act gct ttg gga ttt Gly Arg Leu Asn Pro Ile Ala Asp Leu Glu Thr Thr Ala Leu Gly Phe 305 310 315 320			961
cga ttg ctt cgg ctg cat agg tac aat gta tct cca gcc att ttt gac Arg Leu Leu Arg Leu His Arg Tyr Asn Val Ser Pro Ala Ile Phe Asp 325 330 335			1009
aac ttc aaa gat gcc aat ggg aaa ttc att tgc tcg acc ggt caa ttc Asn Phe Lys Asp Ala Asn Gly Lys Phe Ile Cys Ser Thr Gly Gln Phe 340 345 350			1057
aac aaa gat gta gca agc atg ctg aat ctt tat aga gct tcc cag ctc Asn Lys Asp Val Ala Ser Met Leu Asn Leu Tyr Arg Ala Ser Gln Leu 355 360 365			1105
gca ttt ccc gga gaa aac att ctt gat gaa gct aaa agc ttc gct act Ala Phe Pro Gly Glu Asn Ile Leu Asp Glu Ala Lys Ser Phe Ala Thr 370 375 380			1153
aaa tat ttg aga gaa gct ctt gag aaa agt gag act tcc agt gca tgg Lys Tyr Leu Arg Glu Ala Leu Glu Lys Ser Glu Thr Ser Ser Ala Trp 385 390 395 400			1201
aac aac aaa caa aac ctg agc caa gag atc aaa tac gcg ctg aag act Asn Asn Lys Gln Asn Leu Ser Gln Glu Ile Lys Tyr Ala Leu Lys Thr 405 410 415			1249
tct tgg cat gcc agt gtt ccg aga gtg gaa gca aag aga tac tgt caa Ser Trp His Ala Ser Val Pro Arg Val Glu Ala Lys Arg Tyr Cys Gln 420 425 430			1297
gtg tat cgc cca gat tat gca cgc ata gca aaa tgc gtt tac aag cta Val Tyr Arg Pro Asp Tyr Ala Arg Ile Ala Lys Cys Val Tyr Lys Leu 435 440 445			1345
ccc tac gtg aac aat gaa aag ttt tta gag ctg gga aaa tta gat ttc Pro Tyr Val Asn Asn Glu Lys Phe Leu Glu Leu Gly Lys Leu Asp Phe 450 455 460			1393
aac att atc cag tcc atc cac caa gaa gaa atg aag aat gtt acc agc Asn Ile Ile Gln Ser Ile His Gln Glu Glu Met Lys Asn Val Thr Ser 465 470 475 480			1441
tgg ttt aga gat tcg ggg ttg cca cta ttc acc ttc gct cgg gag agg Trp Phe Arg Asp Ser Gly Leu Pro Leu Phe Thr Phe Ala Arg Glu Arg 485 490 495			1489
ccg ctg gaa ttc tac ttc tta gta gcg gcg ggg acc tat gaa ccc cag Pro Leu Glu Phe Tyr Phe Leu Val Ala Ala Gly Thr Tyr Glu Pro Gln 500 505 510			1537
tat gcc aaa tgc agg ttc ctc ttt aca aaa gtg gca tgc ttg cag act Tyr Ala Lys Cys Arg Phe Leu Phe Thr Lys Val Ala Cys Leu Gln Thr 515 520 525			1585
gtt ctg gac gat atg tat gac act tat gga acc cta gat gaa ttg aag Val Leu Asp Asp Met Tyr Asp Thr Tyr Gly Thr Leu Asp Glu Leu Lys 530 535 540			1633

cta ttc act gag gct gtg aga aga tgg gac ctc tcc ttt aca gaa aac	1681
Leu Phe Thr Glu Ala Val Arg Arg Trp Asp Leu Ser Phe Thr Glu Asn	
545 550 555 560	
ctt cca gac tat atg aaa cta tgt tac caa atc tat tat gac ata gtt	1729
Leu Pro Asp Tyr Met Lys Leu Cys Tyr Gln Ile Tyr Tyr Asp Ile Val	
565 570 575	
cac gag gtg gct tgg gag gca gag aag gaa cag ggg cgt gaa ttg gtc	1777
His Glu Val Ala Trp Glu Ala Glu Lys Glu Gln Gly Arg Glu Leu Val	
580 585 590	
agc ttt ttc aga aag gga tgg gag gat tat ctt ctg ggt tat tat gaa	1825
Ser Phe Phe Arg Lys Gly Trp Glu Asp Tyr Leu Leu Gly Tyr Tyr Glu	
595 600 605	
gaa gct gaa tgg tta gct gct gag tat gtg cct acc ttg gac gag tac	1873
Glu Ala Glu Trp Leu Ala Ala Glu Tyr Val Pro Thr Leu Asp Glu Tyr	
610 615 620	
ata aag aat gga atc aca tct atc ggc caa cgt ata ctt ctg ttg agt	1921
Ile Lys Asn Gly Ile Thr Ser Ile Gly Gln Arg Ile Leu Leu Leu Ser	
625 630 635 640	
gga gtg ttg ata atg gat ggg caa ctc ctt tcg caa gag gca tta gag	1969
Gly Val Leu Ile Met Asp Gly Gln Leu Leu Ser Gln Glu Ala Leu Glu	
645 650 655	
aaa gta gat tat cca gga aga cgt gtt ctc aca gag ctg aat agc ctc	2017
Lys Val Asp Tyr Pro Gly Arg Arg Val Leu Thr Glu Leu Asn Ser Leu	
660 665 670	
att tcc cgc ctg gcg gat gac acg aag aca tat aaa gct gag aag gct	2065
Ile Ser Arg Leu Ala Asp Asp Thr Lys Thr Tyr Lys Ala Glu Lys Ala	
675 680 685	
cgt gga gaa ttg gcg tcc agc att gaa tgt tac atg aaa gac cat cct	2113
Arg Gly Glu Leu Ala Ser Ser Ile Glu Cys Tyr Met Lys Asp His Pro	
690 695 700	
gaa tgt aca gag gaa gag gct ctc gat cac atc tat agc att ctg gag	2161
Glu Cys Thr Glu Glu Glu Ala Leu Asp His Ile Tyr Ser Ile Leu Glu	
705 710 715 720	
ccg gcg gtg aag gaa ctg aca aga gag ttt ctg aag ccc gac gac gtc	2209
Pro Ala Val Lys Glu Leu Thr Arg Glu Phe Leu Lys Pro Asp Asp Val	
725 730 735	
cca ttc gcc tgc aag aag atg ctt ttc gag gag aca aga gtg acg atg	2257
Pro Phe Ala Cys Lys Lys Met Leu Phe Glu Glu Thr Arg Val Thr Met	
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Val Ile Phe Lys Asp Gly Asp Gly Phe Gly Val Ser Lys Leu Glu Val	
755 760 765	
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Lys Asp His Ile Lys Glu Cys Leu Ile Glu Pro Leu Pro Leu	
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Tyr Asp Thr Ala Trp Val Ala Arg Val Pro Ala Ile Asp Gly Ser Ala
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Arg Pro Gln Phe Pro Gln Thr Val Asp Trp Ile Leu Lys Asn Gln Leu
65 70 75 80

Lys Asp Gly Ser Trp Gly Ile Gln Ser His Phe Leu Leu Ser Asp Arg
85 90 95

Leu Leu Ala Thr Leu Ser Cys Val Leu Val Leu Leu Lys Trp Asn Val
100 105 110

Gly Asp Leu Gln Val Glu Gln Gly Ile Glu Phe Ile Lys Ser Asn Leu
115 120 125

Glu Leu Val Lys Asp Glu Thr Asp Gln Asp Ser Leu Val Thr Asp Phe
130 135 140

Glu Ile Ile Phe Pro Ser Leu Leu Arg Glu Ala Gln Ser Leu Arg Leu
145 150 155 160

Gly Leu Pro Tyr Asp Leu Pro Tyr Ile His Leu Leu Gln Thr Lys Arg
165 170 175

Gln Glu Arg Leu Ala Lys Leu Ser Arg Glu Glu Ile Tyr Ala Val Pro
180 185 190

Ser Pro Leu Leu Tyr Ser Leu Glu Gly Ile Gln Asp Ile Val Glu Trp

195

200

205

Glu Arg Ile Met Glu Val Gln Ser Gln Asp Gly Ser Phe Leu Ser Ser
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Pro Ala Ser Thr Ala Cys Val Phe Met His Thr Gly Asp Ala Lys Cys
 225 230 235 240

Leu Glu Phe Leu Asn Ser Val Met Ile Lys Phe Gly Asn Phe Val Pro
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Cys Leu Tyr Pro Val Asp Leu Leu Glu Arg Leu Leu Ile Val Asp Asn
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Ile Val Arg Leu Gly Ile Tyr Arg His Phe Glu Lys Glu Ile Lys Glu
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Ala Leu Asp Tyr Val Tyr Arg His Trp Asn Glu Arg Gly Ile Gly Trp
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Gly Arg Leu Asn Pro Ile Ala Asp Leu Glu Thr Thr Ala Leu Gly Phe
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Arg Leu Leu Arg Leu His Arg Tyr Asn Val Ser Pro Ala Ile Phe Asp
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Asn Phe Lys Asp Ala Asn Gly Lys Phe Ile Cys Ser Thr Gly Gln Phe
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Asn Lys Asp Val Ala Ser Met Leu Asn Leu Tyr Arg Ala Ser Gln Leu
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Ala Phe Pro Gly Glu Asn Ile Leu Asp Glu Ala Lys Ser Phe Ala Thr
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Lys Tyr Leu Arg Glu Ala Leu Glu Lys Ser Glu Thr Ser Ser Ala Trp
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Asn Asn Lys Gln Asn Leu Ser Gln Glu Ile Lys Tyr Ala Leu Lys Thr
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Ser Trp His Ala Ser Val Pro Arg Val Glu Ala Lys Arg Tyr Cys Gln
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Val Tyr Arg Pro Asp Tyr Ala Arg Ile Ala Lys Cys Val Tyr Lys Leu
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Pro Tyr Val Asn Asn Glu Lys Phe Leu Glu Leu Gly Lys Leu Asp Phe
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Asn Ile Ile Gln Ser Ile His Gln Glu Glu Met Lys Asn Val Thr Ser
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Trp Phe Arg Asp Ser Gly Leu Pro Leu Phe Thr Phe Ala Arg Glu Arg
485 490 495

Pro Leu Glu Phe Tyr Phe Leu Val Ala Ala Gly Thr Tyr Glu Pro Gln
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Tyr Ala Lys Cys Arg Phe Leu Phe Thr Lys Val Ala Cys Leu Gln Thr
515 520 525

Val Leu Asp Asp Met Tyr Asp Thr Tyr Gly Thr Leu Asp Glu Leu Lys
530 535 540

Leu Phe Thr Glu Ala Val Arg Arg Trp Asp Leu Ser Phe Thr Glu Asn
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Leu Pro Asp Tyr Met Lys Leu Cys Tyr Gln Ile Tyr Tyr Asp Ile Val
565 570 575

His Glu Val Ala Trp Glu Ala Glu Lys Glu Gln Gly Arg Glu Leu Val
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Ser Phe Phe Arg Lys Gly Trp Glu Asp Tyr Leu Leu Gly Tyr Tyr Glu
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Glu Ala Glu Trp Leu Ala Ala Glu Tyr Val Pro Thr Leu Asp Glu Tyr
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Ile Lys Asn Gly Ile Thr Ser Ile Gly Gln Arg Ile Leu Leu Leu Ser
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Gly Val Leu Ile Met Asp Gly Gln Leu Leu Ser Gln Glu Ala Leu Glu
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Lys Val Asp Tyr Pro Gly Arg Arg Val Leu Thr Glu Leu Asn Ser Leu
660 665 670

Ile Ser Arg Leu Ala Asp Asp Thr Lys Thr Tyr Lys Ala Glu Lys Ala
675 680 685

Arg Gly Glu Leu Ala Ser Ser Ile Glu Cys Tyr Met Lys Asp His Pro
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Glu Cys Thr Glu Glu Glu Ala Leu Asp His Ile Tyr Ser Ile Leu Glu
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725 730 735

Pro Phe Ala Cys Lys Lys Met Leu Phe Glu Glu Thr Arg Val Thr Met
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Val Trp Asp Asp Asp Leu Ile His Ser Leu Asn Ser Pro Tyr Gly Ala
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cct gca tat tat gag ctc ctt caa aag ctt att gag gag atc aag cat 143
Pro Ala Tyr Tyr Glu Leu Leu Gln Lys Leu Ile Glu Glu Ile Lys His
35 40 45

tta ctt ttg act gaa atg gaa atg gat gat ggc gat cat gat tta atc 191
Leu Leu Leu Thr Glu Met Glu Met Asp Asp Gly Asp His Asp Leu Ile
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Lys Arg Leu Gln Ile Val Asp Thr Leu Glu Cys Leu Gly Ile Asp Arg
65 70 75

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His Phe Glu His Glu Ile Gln Thr Ala Ala Leu Asp Tyr Val Tyr Arg
80 85 90 95

tgg tgg aac gaa aaa ggt atc ggg gag gga tca aga gat tcc ttc agc	335
Trp Trp Asn Glu Lys Gly Ile Gly Glu Gly Ser Arg Asp Ser Phe Ser	
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Lys Asp Leu Asn Ala Thr Ala Leu Gly Phe Arg Ala Leu Arg Leu His	
115 120 125	
cga tat aac gta tcg tca ggt gtg ttg aag aat ttc aag gat gaa aac	431
Arg Tyr Asn Val Ser Ser Gly Val Leu Lys Asn Phe Lys Asp Glu Asn	
130 135 140	
ggg aag ttc ttc tgc aac ttt act ggt gaa gaa gga aga gga gat aaa	479
Gly Lys Phe Phe Cys Asn Phe Thr Gly Glu Glu Gly Arg Gly Asp Lys	
145 150 155	
caa gtg aga agc atg ttg tcg tta ctt cga gct tca gag att tcg ttt	527
Gln Val Arg Ser Met Leu Ser Leu Leu Arg Ala Ser Glu Ile Ser Phe	
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ccc gga gaa aaa gtg atg gaa gag gcc aag gca ttc aca aga gaa tat	575
Pro Gly Glu Lys Val Met Glu Glu Ala Lys Ala Phe Thr Arg Glu Tyr	
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Leu Asn Gln Val Leu Ala Gly His Gly Asp Val Thr Asp Val Asp Gln	
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agc ctt ttg gag aga ggt gaa gta cgc att gga gtt tcc atg gct tgc	671
Ser Leu Leu Glu Arg Gly Glu Val Arg Ile Gly Val Ser Met Ala Cys	
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Ser Val Pro Arg Trp Glu Ala Arg Ser Phe Leu Glu Ile Tyr Gly His	
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Asn His Ser Trp Leu Lys Ser Asn Ile Asn Gln Lys Met Leu Lys Leu	
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Ala Lys Leu Asp Phe Asn Ile Leu Gln Cys Lys His His Lys Glu Ile	
260 265 270	
cag ttt att aca agg tgg tgg aga gac tcg ggt ata tcg cag ctg aat	863
Gln Phe Ile Thr Arg Trp Trp Arg Asp Ser Gly Ile Ser Gln Leu Asn	
275 280 285	
ttc tat cga aag cga cac gtg gaa tat tat tct tgg gtt gtt atg tgc	911
Phe Tyr Arg Lys Arg His Val Glu Tyr Tyr Ser Trp Val Val Met Cys	
290 295 300	
att ttt gag cca gag ttc tct gaa agt aga att gcc ttc gcc aaa act	959
Ile Phe Glu Pro Glu Phe Ser Glu Ser Arg Ile Ala Phe Ala Lys Thr	
305 310 315	
gct atc cta tgt act gtt cta gat gac ctc tat gat acg cac gca acg	1007
Ala Ile Leu Cys Thr Val Leu Asp Asp Leu Tyr Asp Thr His Ala Thr	
320 325 330 335	
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Ser	Leu	Thr	Asp	Asp	Leu	Pro	Asp	Tyr	Ile	Lys	Ile	Ala	Phe	Gln	Phe	
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Phe	Phe	Asn	Thr	Val	Asn	Glu	Leu	Ile	Val	Glu	Ile	Val	Lys	Arg	Gln	
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Gly	Arg	Asp	Met	Thr	Thr	Ile	Val	Lys	Asp	Cys	Trp	Lys	Arg	Tyr	Ile	
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gag	tct	tat	ctg	caa	gaa	gcg	gaa	tgg	ata	gca	act	gga	cat	att	ccc	1247
Glu	Ser	Tyr	Leu	Gln	Glu	Ala	Glu	Trp	Ile	Ala	Thr	Gly	His	Ile	Pro	
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Thr	Phe	Asn	Glu	Tyr	Ile	Lys	Asn	Gly	Met	Ala	Ser	Ser	Gly	Met	Cys	
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Ile	Val	Asn	Leu	Asn	Pro	Leu	Leu	Leu	Leu	Gly	Lys	Leu	Leu	Pro	Asp	
			435					440					445			
aac	att	ctg	gag	caa	ata	cat	tct	cca	tcc	aag	atc	ctg	gac	ctc	tta	1391
Asn	Ile	Leu	Glu	Gln	Ile	His	Ser	Pro	Ser	Lys	Ile	Leu	Asp	Leu	Leu	
		450					455					460				
gaa	ttg	acg	ggc	aga	atc	gcc	gat	gac	tta	aaa	gat	ttc	gag	gac	gag	1439
Glu	Leu	Thr	Gly	Arg	Ile	Ala	Asp	Asp	Leu	Lys	Asp	Phe	Glu	Asp	Glu	
	465					470					475					
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Lys	Glu	Arg	Gly	Glu	Met	Ala	Ser	Ser	Leu	Gln	Cys	Tyr	Met	Lys	Glu	
480					485					490					495	
aat	cct	gaa	tct	aca	gtg	gaa	aat	gct	tta	aat	cac	ata	aaa	ggc	atc	1535
Asn	Pro	Glu	Ser	Thr	Val	Glu	Asn	Ala	Leu	Asn	His	Ile	Lys	Gly	Ile	
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ctt	aat	cgt	tcc	ctt	gag	gaa	ttt	aat	tgg	gag	ttt	atg	aag	cag	gat	1583
Leu	Asn	Arg	Ser	Leu	Glu	Glu	Phe	Asn	Trp	Glu	Phe	Met	Lys	Gln	Asp	
			515					520					525			
agt	gtc	cca	atg	tgt	tgc	aag	aaa	ttc	act	ttc	aat	ata	ggt	cga	gga	1631
Ser	Val	Pro	Met	Cys	Cys	Lys	Lys	Phe	Thr	Phe	Asn	Ile	Gly	Arg	Gly	
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Leu	Gln	Phe	Ile	Tyr	Lys	Tyr	Arg	Asp	Gly	Leu						

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Leu Leu Thr Glu Met Glu Met Asp Asp Gly Asp His Asp Leu Ile Lys
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Arg Leu Gln Ile Val Asp Thr Leu Glu Cys Leu Gly Ile Asp Arg His
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Phe Glu His Glu Ile Gln Thr Ala Ala Leu Asp Tyr Val Tyr Arg Trp
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Trp Asn Glu Lys Gly Ile Gly Glu Gly Ser Arg Asp Ser Phe Ser Lys
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Asp Leu Asn Ala Thr Ala Leu Gly Phe Arg Ala Leu Arg Leu His Arg
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Tyr Asn Val Ser Ser Gly Val Leu Lys Asn Phe Lys Asp Glu Asn Gly
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Lys Phe Phe Cys Asn Phe Thr Gly Glu Glu Gly Arg Gly Asp Lys Gln
 145 150 155 160

Val Arg Ser Met Leu Ser Leu Leu Arg Ala Ser Glu Ile Ser Phe Pro
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Gly Glu Lys Val Met Glu Glu Ala Lys Ala Phe Thr Arg Glu Tyr Leu
180 185 190

Asn Gln Val Leu Ala Gly His Gly Asp Val Thr Asp Val Asp Gln Ser
195 200 205

Leu Leu Glu Arg Gly Glu Val Arg Ile Gly Val Ser Met Ala Cys Ser
210 215 220

Val Pro Arg Trp Glu Ala Arg Ser Phe Leu Glu Ile Tyr Gly His Asn
225 230 235 240

His Ser Trp Leu Lys Ser Asn Ile Asn Gln Lys Met Leu Lys Leu Ala
245 250 255

Lys Leu Asp Phe Asn Ile Leu Gln Cys Lys His His Lys Glu Ile Gln
260 265 270

Phe Ile Thr Arg Trp Trp Arg Asp Ser Gly Ile Ser Gln Leu Asn Phe
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Tyr Arg Lys Arg His Val Glu Tyr Tyr Ser Trp Val Val Met Cys Ile
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Phe Glu Pro Glu Phe Ser Glu Ser Arg Ile Ala Phe Ala Lys Thr Ala
305 310 315 320

Ile Leu Cys Thr Val Leu Asp Asp Leu Tyr Asp Thr His Ala Thr Leu
325 330 335

His Glu Ile Lys Ile Met Thr Glu Gly Val Arg Arg Trp Asp Leu Ser
340 345 350

Leu Thr Asp Asp Leu Pro Asp Tyr Ile Lys Ile Ala Phe Gln Phe Phe
355 360 365

Phe Asn Thr Val Asn Glu Leu Ile Val Glu Ile Val Lys Arg Gln Gly
370 375 380

Arg Asp Met Thr Thr Ile Val Lys Asp Cys Trp Lys Arg Tyr Ile Glu
385 390 395 400

Ser Tyr Leu Gln Glu Ala Glu Trp Ile Ala Thr Gly His Ile Pro Thr
405 410 415

Phe Asn Glu Tyr Ile Lys Asn Gly Met Ala Ser Ser Gly Met Cys Ile
 420 425 430

Val Asn Leu Asn Pro Leu Leu Leu Leu Gly Lys Leu Leu Pro Asp Asn
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Ile Leu Glu Gln Ile His Ser Pro Ser Lys Ile Leu Asp Leu Leu Glu
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Leu Thr Gly Arg Ile Ala Asp Asp Leu Lys Asp Phe Glu Asp Glu Lys
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Glu Arg Gly Glu Met Ala Ser Ser Leu Gln Cys Tyr Met Lys Glu Asn
 485 490 495

Pro Glu Ser Thr Val Glu Asn Ala Leu Asn His Ile Lys Gly Ile Leu
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Asn Arg Ser Leu Glu Glu Phe Asn Trp Glu Phe Met Lys Gln Asp Ser
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Val Pro Met Cys Cys Lys Lys Phe Thr Phe Asn Ile Gly Arg Gly Leu
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Gln Phe Ile Tyr Lys Tyr Arg Asp Gly Leu Tyr Ile Ser Asp Lys Glu
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47

95

Lys	Val	Leu	Ala	Gly	Arg	Glu	Ala	Thr	His	Val	Asp	Glu	Ser	Leu	Leu	
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Gly	Glu	Val	Lys	Tyr	Ala	Leu	Glu	Phe	Pro	Trp	His	Cys	Ser	Val	Gln	
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aga	tgg	gag	gca	agg	agc	ttt	atc	gaa	ata	ttt	gga	caa	att	gat	tca	191
Arg	Trp	Glu	Ala	Arg	Ser	Phe	Ile	Glu	Ile	Phe	Gly	Gln	Ile	Asp	Ser	
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Glu	Leu	Lys	Ser	Asn	Leu	Ser	Lys	Lys	Met	Leu	Glu	Leu	Ala	Lys	Leu	
	65					70					75					
gac	ttc	aat	att	ctg	caa	tgc	aca	cat	cag	aaa	gaa	ctg	cag	att	atc	287
Asp	Phe	Asn	Ile	Leu	Gln	Cys	Thr	His	Gln	Lys	Glu	Leu	Gln	Ile	Ile	
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tca	agg	tgg	ttc	gca	gac	tca	agt	ata	gca	tcc	ctg	aat	ttc	tat	cgg	335
Ser	Arg	Trp	Phe	Ala	Asp	Ser	Ser	Ile	Ala	Ser	Leu	Asn	Phe	Tyr	Arg	
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Lys	Cys	Tyr	Val	Glu	Phe	Tyr	Phe	Trp	Met	Ala	Ala	Ala	Ile	Ser	Glu	
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Pro	Glu	Phe	Ser	Gly	Ser	Arg	Val	Ala	Phe	Thr	Lys	Ile	Ala	Ile	Leu	
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Met	Thr	Met	Leu	Asp	Asp	Leu	Tyr	Asp	Thr	His	Gly	Thr	Leu	Asp	Gln	
		145				150					155					
ctc	aaa	atc	ttt	aca	gag	gga	gtg	aga	cga	tgg	gat	gtt	tcg	ttg	gta	527
Leu	Lys	Ile	Phe	Thr	Glu	Gly	Val	Arg	Arg	Trp	Asp	Val	Ser	Leu	Val	
	160				165				170						175	
gag	ggc	ctc	cca	gac	ttc	atg	aaa	att	gca	ttc	gag	ttc	tgg	tta	aag	575
Glu	Gly	Leu	Pro	Asp	Phe	Met	Lys	Ile	Ala	Phe	Glu	Phe	Trp	Leu	Lys	
				180					185					190		
aca	tct	aat	gaa	ttg	att	gct	gaa	gct	gtt	aaa	gcg	caa	ggg	caa	gat	623
Thr	Ser	Asn	Glu	Leu	Ile	Ala	Glu	Ala	Val	Lys	Ala	Gln	Gly	Gln	Asp	
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Met	Ala	Ala	Tyr	Ile	Arg	Lys	Asn	Ala	Trp	Glu	Arg	Tyr	Leu	Glu	Ala	
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Tyr	Leu	Gln	Asp	Ala	Glu	Trp	Ile	Ala	Thr	Gly	His	Val	Pro	Thr	Phe	
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gat	gag	tac	ttg	aat	aat	ggc	aca	cca	aac	act	ggg	atg	tgt	gta	ttg	767
Asp	Glu	Tyr	Leu	Asn	Asn	Gly	Thr	Pro	Asn	Thr	Gly	Met	Cys	Val	Leu	
					245					250					255	
aat	ttg	att	ccg	ctt	ctg	tta	atg	ggg	gaa	cat	tta	cca	atc	gac	att	815
Asn	Leu	Ile	Pro	Leu	Leu	Leu	Met	Gly	Glu	His	Leu	Pro	Ile	Asp	Ile	

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Leu Glu Gln Ile Phe Leu Pro Ser Arg	Phe His His Leu Ile Glu Leu		
275	280	285	
gct tcc agg ctc gtc gat gac gcg aga gat	ttc cag gcg gag aag gat	911	
Ala Ser Arg Leu Val Asp Asp Ala Arg Asp	Phe Gln Ala Glu Lys Asp		
290	295	300	
cat ggg gat tta tcg tgt att gag tgt tat	tta aaa gat cat cct gag	959	
His Gly Asp Leu Ser Cys Ile Glu Cys Tyr	Leu Lys Asp His Pro Glu		
305	310	315	
tct aca gta gaa gat gct tta aat cat gtt	aat ggc ctc ctt ggc aat	1007	
Ser Thr Val Glu Asp Ala Leu Asn His Val	Asn Gly Leu Leu Gly Asn		
320	325	330	
tgc ctt ctg gaa atg aat tgg aag ttc tta	aag aag cag gac agt gtg	1055	
Cys Leu Leu Glu Met Asn Trp Lys Phe Leu	Lys Lys Gln Asp Ser Val		
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cca ctc tcg tgt aag aag tac agc ttc cat	gta ttg gca cga agc atc	1103	
Pro Leu Ser Cys Lys Lys Tyr Ser Phe His	Val Leu Ala Arg Ser Ile		
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caa ttc atg tac aat caa ggc gat ggc ttc	tcc att tcg aac aaa gtg	1151	
Gln Phe Met Tyr Asn Gln Gly Asp Gly Phe	Ser Ile Ser Asn Lys Val		
370	375	380	
atc aag gat caa gtg cag aaa gtt ctt att	gtc ccc gtg cct att tga	1199	
Ile Lys Asp Gln Val Gln Lys Val Leu Ile	Val Pro Val Pro Ile		
385	390	395	
tagtagatac tagatagtag attagtagct attagtattt	atttcatatc aatatttact	1259	
aatgctgatg atggttaaag tccattcaga ccaatctttg	gtttattgga cttaaataaa	1319	
tgaattaatt agtttgtttt aaaattgtac tatttactgt	tggaataaat gttttcatta	1379	
ttgaaataac tagcacaact atttttagtgt ggttgat		1416	

<210> 20
 <211> 398
 <212> PRT
 <213> Abies Grandis

<400> 20

Lys Val Met Glu Glu Ala Lys Ala Phe Thr Thr Asn Tyr Leu Lys Lys
1 5 10 15

Val Leu Ala Gly Arg Glu Ala Thr His Val Asp Glu Ser Leu Leu Gly
20 25 30

Glu Val Lys Tyr Ala Leu Glu Phe Pro Trp His Cys Ser Val Gln Arg
35 40 45

Trp Glu Ala Arg Ser Phe Ile Glu Ile Phe Gly Gln Ile Asp Ser Glu
50 55 60

Leu Lys Ser Asn Leu Ser Lys Lys Met Leu Glu Leu Ala Lys Leu Asp
65 70 75 80

Phe Asn Ile Leu Gln Cys Thr His Gln Lys Glu Leu Gln Ile Ile Ser
85 90 95

Arg Trp Phe Ala Asp Ser Ser Ile Ala Ser Leu Asn Phe Tyr Arg Lys
100 105 110

Cys Tyr Val Glu Phe Tyr Phe Trp Met Ala Ala Ala Ile Ser Glu Pro
115 120 125

Glu Phe Ser Gly Ser Arg Val Ala Phe Thr Lys Ile Ala Ile Leu Met
130 135 140

Thr Met Leu Asp Asp Leu Tyr Asp Thr His Gly Thr Leu Asp Gln Leu
145 150 155 160

Lys Ile Phe Thr Glu Gly Val Arg Arg Trp Asp Val Ser Leu Val Glu
165 170 175

Gly Leu Pro Asp Phe Met Lys Ile Ala Phe Glu Phe Trp Leu Lys Thr
180 185 190

Ser Asn Glu Leu Ile Ala Glu Ala Val Lys Ala Gln Gly Gln Asp Met
195 200 205

Ala Ala Tyr Ile Arg Lys Asn Ala Trp Glu Arg Tyr Leu Glu Ala Tyr
210 215 220

Leu Gln Asp Ala Glu Trp Ile Ala Thr Gly His Val Pro Thr Phe Asp
225 230 235 240

Glu Tyr Leu Asn Asn Gly Thr Pro Asn Thr Gly Met Cys Val Leu Asn
245 250 255

Leu Ile Pro Leu Leu Leu Met Gly Glu His Leu Pro Ile Asp Ile Leu
260 265 270

Glu Gln Ile Phe Leu Pro Ser Arg Phe His His Leu Ile Glu Leu Ala
275 280 285

Ser Arg Leu Val Asp Asp Ala Arg Asp Phe Gln Ala Glu Lys Asp His
290 295 300

Gly Asp Leu Ser Cys Ile Glu Cys Tyr Leu Lys Asp His Pro Glu Ser
305 310 315 320

Thr Val Glu Asp Ala Leu Asn His Val Asn Gly Leu Leu Gly Asn Cys
325 330 335

Leu Leu Glu Met Asn Trp Lys Phe Leu Lys Lys Gln Asp Ser Val Pro
340 345 350

Leu Ser Cys Lys Lys Tyr Ser Phe His Val Leu Ala Arg Ser Ile Gln
355 360 365

Phe Met Tyr Asn Gln Gly Asp Gly Phe Ser Ile Ser Asn Lys Val Ile
370 375 380

Lys Asp Gln Val Gln Lys Val Leu Ile Val Pro Val Pro Ile
385 390 395

<210> 21
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Oligonucleotide PCR Primer E

<220>
<221> misc_feature
<222> (1)..(23)
<223> Wherein N=inosine residue

<400> 21
ggngaramrr tnatggarga rgc

23

<210> 22
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Degenerate Oligonucleotide Primer F

<220>
<221> misc_feature
<222> (1)..(24)
<223> Wherein N=inosine residue

<400> 22

garytn Cary tnhbnmgntg gtgg

24

<210> 23
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Degenerate Oligonucleotide Primer G

<220>
<221> misc_feature
<222> (1)..(21)
<223> Wherein N=inosine residue

<400> 23
ccarttnarn ccyttnacrt c

21

<210> 24
<211> 533
<212> DNA
<213> Abies Grandis

<400> 24
ggggaaaaaa tgatggagga agctgaaatc ttctctacca aatatttaaa agaagccctg 60
caaaagattc cggctctccag tctttcgcga gagatcgggg acgttttgga atatggttgg 120
cacacatatt tgccgcgatt ggaagcaagg aattacatcc aagtcttttg acaggacact 180
gagaacacga agtcatatgt gaagagcaaa aaacttttag aactcgcaaa attggagttc 240
aacatctttc aatccttact cgcatatccg cattgcaacc cattctgaca atggacatcc 300
cctttcctga tcatatcctc aaggaagttg acttcccac aaagcttaac gacttggcat 360
gtgccatcct tcgattacga ggtgatacgc ggtgctacaa ggcggacagg gctcgtggag 420
aagaagcttc ctctatatca tggtatatga aagacaatcc tggagtatca gaggaagatg 480
ctctcgatca tatcaacgcc atgatcagtg acgaagtcaa aggcttcaat tgg 533

<210> 25
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Conserved Amino Acid Motif on Which the Sequence of Primer D is based

<220>
<221> MISC_FEATURE
<222> (3)..(3)
<223> Wherein Xaa=THR or ILE

<220>
<221> MISC_FEATURE
<222> (4)..(4)
<223> Wherein Xaa=ILE or TYR or PHE

<220>
<221> MISC_FEATURE
<222> (6)..(6)
<223> Wherein Xaa=ALA or VAL

<220>
<221> MISC_FEATURE
<222> (8)..(8)
<223> Wherein Xaa=ALA or GLY

<400> 25

Asp Asp Xaa Xaa Asp Xaa Tyr Xaa
1 5

<210> 26
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Conserved Amino Acid Motif on Which the Sequence of Primer E is based

<220>
<221> MISC_FEATURE
<222> (3)..(3)
<223> Wherein Xaa=LYS or THR

<220>
<221> MISC_FEATURE
<222> (4)..(4)
<223> Wherein Xaa=VAL or ILE

<220>
<221> MISC_FEATURE
<222> (6)..(6)
<223> Wherein Xaa=GLU or ASP

<400> 26

Gly Glu Xaa Xaa Met Xaa Glu Ala
1 5

<210> 27
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Conserved Amino Acid on Which the Sequence of Primer F is based

<220>
<221> MISC_FEATURE
<222> (2)..(2)
<223> Wherein Xaa=PHE or TYR or ASP

<220>
<221> MISC_FEATURE
<222> (3)..(3)
<223> Wherein Xaa=ILE or LEU

<220>
<221> MISC_FEATURE
<222> (4)..(4)
<223> Wherein Xaa=THR or LEU or ARG

<400> 27

Gln Xaa Xaa Xaa Arg Trp Trp
1 5

<210> 28
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Conserved Amino Acid Motif on Which the Sequence of Primer G is based

<220>
<221> MISC_FEATURE
<222> (6)..(6)
<223> Wherein Xaa=PHE or LEU

<400> 28

Asp Val Ile Lys Gly Xaa Asn Trp
1 5

<210> 29
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> T3 Primer Oligonucleotide

<400> 29
aattaaccct cactaaaggg

<210> 30
 <211> 22
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> T7 Primer Oligonucleotide

<400> 30
 gtaatacgac tcactatagg gc

22

<210> 31
 <211> 2205
 <212> DNA
 <213> Abies Grandis

<220>
 <221> CDS
 <222> (57)..(1943)
 <223>

<400> 31
 gttatcttga gcttcctcca tataggccaa cacatatcat atcaaaggga gcaaga atg 59
 Met
 1

gct ctg gtt tct atc tca ccg ttg gct tcg aaa tct tgc ctg cgc aag 107
 Ala Leu Val Ser Ile Ser Pro Leu Ala Ser Lys Ser Cys Leu Arg Lys
 5 10 15

tcg ttg atc agt tca att cat gaa cat aag cct ccc tat aga aca atc 155
 Ser Leu Ile Ser Ser Ile His Glu His Lys Pro Pro Tyr Arg Thr Ile
 20 25 30

cca aat ctt gga atg cgt agg cga ggg aaa tct gtc acg cct tcc atg 203
 Pro Asn Leu Gly Met Arg Arg Arg Gly Lys Ser Val Thr Pro Ser Met
 35 40 45

agc atc agt ttg gcc acc gct gca cct gat gat ggt gta caa aga cgc 251
 Ser Ile Ser Leu Ala Thr Ala Ala Pro Asp Asp Gly Val Gln Arg Arg
 50 55 60 65

ata ggt gac tac cat tcc aat atc tgg gac gat gat ttc ata cag tct 299
 Ile Gly Asp Tyr His Ser Asn Ile Trp Asp Asp Asp Phe Ile Gln Ser
 70 75 80

cta tca acg cat tat ggg gaa ccc tct tac cag gaa cgt gct gag aga 347
 Leu Ser Thr His Tyr Gly Glu Pro Ser Tyr Gln Glu Arg Ala Glu Arg
 85 90 95

tta att gtg gag gta aag aag ata ttc aat tca atg tac ctg gat gat 395
 Leu Ile Val Glu Val Lys Lys Ile Phe Asn Ser Met Tyr Leu Asp Asp
 100 105 110

gga aga tta atg agt tcc ttt aat gat ctc atg caa cgc ctt tgg ata 443
 Gly Arg Leu Met Ser Ser Phe Asn Asp Leu Met Gln Arg Leu Trp Ile
 115 120 125

gtc gat agc gtt gaa cgt ttg ggg ata gct aga cat ttc aag aac gag 491

Val Asp Ser Val Glu Arg Leu Gly Ile Ala Arg His Phe Lys Asn Glu	
130 135 140 145	
ata aca tca gct ctg gat tat gtt ttc cgt tac tgg gag gaa aac ggc	539
Ile Thr Ser Ala Leu Asp Tyr Val Phe Arg Tyr Trp Glu Glu Asn Gly	
150 155 160	
att gga tgt ggg aga gac agt att gtt act gat ctc aac tca act gcg	587
Ile Gly Cys Gly Arg Asp Ser Ile Val Thr Asp Leu Asn Ser Thr Ala	
165 170 175	
ttg ggg ttt cga act ctt cga tta cac ggg tac act gta tct cca gag	635
Leu Gly Phe Arg Thr Leu Arg Leu His Gly Tyr Thr Val Ser Pro Glu	
180 185 190	
gtt tta aaa gct ttt caa gat caa aat gga cag ttt gta tgc tcc ccc	683
Val Leu Lys Ala Phe Gln Asp Gln Asn Gly Gln Phe Val Cys Ser Pro	
195 200 205	
ggt cag aca gag ggt gag atc aga agc gtt ctt aac tta tat cgg gct	731
Gly Gln Thr Glu Gly Glu Ile Arg Ser Val Leu Asn Leu Tyr Arg Ala	
210 215 220 225	
tcc ctc att gcc ttc cct ggt gag aaa gtt atg gaa gaa gct gaa atc	779
Ser Leu Ile Ala Phe Pro Gly Glu Lys Val Met Glu Glu Ala Glu Ile	
230 235 240	
ttc tcc aca aga tat ttg aaa gaa gct cta caa aag att cca gtc tcc	827
Phe Ser Thr Arg Tyr Leu Lys Glu Ala Leu Gln Lys Ile Pro Val Ser	
245 250 255	
gct ctt tca caa gag ata aag ttt gtt atg gaa tat ggc tgg cac aca	875
Ala Leu Ser Gln Glu Ile Lys Phe Val Met Glu Tyr Gly Trp His Thr	
260 265 270	
aat ttg cca aga ttg gaa gca aga aat tac ata gac aca ctt gag aaa	923
Asn Leu Pro Arg Leu Glu Ala Arg Asn Tyr Ile Asp Thr Leu Glu Lys	
275 280 285	
gac acc agt gca tgg ctc aat aaa aat gct ggg aag aag ctt tta gaa	971
Asp Thr Ser Ala Trp Leu Asn Lys Asn Ala Gly Lys Lys Leu Leu Glu	
290 295 300 305	
ctt gca aaa ttg gag ttc aat ata ttt aac tcc tta caa caa aag gaa	1019
Leu Ala Lys Leu Glu Phe Asn Ile Phe Asn Ser Leu Gln Gln Lys Glu	
310 315 320	
tta caa tat ctt ttg aga tgg tgg aaa gag tcg gat ttg cct aaa ttg	1067
Leu Gln Tyr Leu Leu Arg Trp Trp Lys Glu Ser Asp Leu Pro Lys Leu	
325 330 335	
aca ttt gct cgg cat cgt cat gtg gaa ttc tac act ttg gcc tct tgt	1115
Thr Phe Ala Arg His Arg His Val Glu Phe Tyr Thr Leu Ala Ser Cys	
340 345 350	
att gcc att gac cca aaa cat tct gca ttc aga cta ggc ttc gcc aaa	1163
Ile Ala Ile Asp Pro Lys His Ser Ala Phe Arg Leu Gly Phe Ala Lys	
355 360 365	
atg tgt cat ctt gtc aca gtt ttg gac gat att tac gac act ttt gga	1211
Met Cys His Leu Val Thr Val Leu Asp Asp Ile Tyr Asp Thr Phe Gly	

370	375	380	385	
acg att gac gag ctt gaa ctc ttc aca tct gca att aag aga tgg aat				1259
Thr Ile Asp Glu Leu Glu Leu Phe Thr Ser Ala Ile Lys Arg Trp Asn				
	390	395	400	
tca tca gag ata gaa cac ctt cca gaa tat atg aaa tgt gtg tac atg				1307
Ser Ser Glu Ile Glu His Leu Pro Glu Tyr Met Lys Cys Val Tyr Met				
	405	410	415	
gtc gtg ttt gaa act gta aat gaa ctg aca cga gag gcg gag aag act				1355
Val Val Phe Glu Thr Val Asn Glu Leu Thr Arg Glu Ala Glu Lys Thr				
	420	425	430	
caa ggg aga aac act ctc aac tat gtt cga aag gct tgg gag gct tat				1403
Gln Gly Arg Asn Thr Leu Asn Tyr Val Arg Lys Ala Trp Glu Ala Tyr				
	435	440	445	
ttt gat tca tat atg gaa gaa gca aaa tgg atc tct aat ggt tat ctg				1451
Phe Asp Ser Tyr Met Glu Glu Ala Lys Trp Ile Ser Asn Gly Tyr Leu				
	450	455	460	465
cca acg ttt gaa gag tac cat gag aat ggg aaa gtg agc tct gca tat				1499
Pro Thr Phe Glu Glu Tyr His Glu Asn Gly Lys Val Ser Ser Ala Tyr				
	470	475	480	
cgc gta gca aca ttg caa ccc atc ctc act ttg aat gca tgg ctt cct				1547
Arg Val Ala Thr Leu Gln Pro Ile Leu Thr Leu Asn Ala Trp Leu Pro				
	485	490	495	
gat tac atc ttg aag gga att gat ttt cca tcc agg ttc aat gat ttg				1595
Asp Tyr Ile Leu Lys Gly Ile Asp Phe Pro Ser Arg Phe Asn Asp Leu				
	500	505	510	
gca tcg tcc ttc ctt cgg cta cga ggt gac aca cgc tgc tac aag gcc				1643
Ala Ser Ser Phe Leu Arg Leu Arg Gly Asp Thr Arg Cys Tyr Lys Ala				
	515	520	525	
gat agg gat cgt ggt gaa gaa gct tcg tgt ata tca tgt tat atg aaa				1691
Asp Arg Asp Arg Gly Glu Glu Ala Ser Cys Ile Ser Cys Tyr Met Lys				
	530	535	540	545
gac aat cct gga tca acc gaa gaa gat gcc ctc aat cat atc aat gcc				1739
Asp Asn Pro Gly Ser Thr Glu Glu Asp Ala Leu Asn His Ile Asn Ala				
	550	555	560	
atg gtc aat gac ata atc aaa gaa tta aat tgg gaa ctt cta aga tcc				1787
Met Val Asn Asp Ile Ile Lys Glu Leu Asn Trp Glu Leu Leu Arg Ser				
	565	570	575	
aac gac aat att cca atg ctg gcc aag aaa cat gct ttt gac ata aca				1835
Asn Asp Asn Ile Pro Met Leu Ala Lys Lys His Ala Phe Asp Ile Thr				
	580	585	590	
aga gct ctc cac cat ctc tac ata tat cga gat ggc ttt agt gtt gcc				1883
Arg Ala Leu His His Leu Tyr Ile Tyr Arg Asp Gly Phe Ser Val Ala				
	595	600	605	
aac aag gaa aca aaa aaa ttg gtt atg gaa aca ctc ctt gaa tct atg				1931
Asn Lys Glu Thr Lys Lys Leu Val Met Glu Thr Leu Leu Glu Ser Met				
	610	615	620	625

ctt ttt taa cta taaccatata cataataata agtcataat gctaaattat 1983
 Leu Phe Leu

tggccttatg acatagttta tgtatgtact tgtgtgaatt caatcatata gtgtgggtat 2043
 gattaaaaag ctagagctta ctaggttagt aacatgggtga taaaagttat aaaatgtgag 2103
 ttatagagat acccatgttg aataatgaat tacaaaaaga gaaatttatg tagaataaga 2163
 ttggaagctt ttcaattggt ttaaaaaaaaa aaaaaaaaaa aa 2205

<210> 32
 <211> 627
 <212> PRT
 <213> Abies Grandis

<400> 32

Met Ala Leu Val Ser Ile Ser Pro Leu Ala Ser Lys Ser Cys Leu Arg
 1 5 10 15

Lys Ser Leu Ile Ser Ser Ile His Glu His Lys Pro Pro Tyr Arg Thr
 20 25 30

Ile Pro Asn Leu Gly Met Arg Arg Arg Gly Lys Ser Val Thr Pro Ser
 35 40 45

Met Ser Ile Ser Leu Ala Thr Ala Ala Pro Asp Asp Gly Val Gln Arg
 50 55 60

Arg Ile Gly Asp Tyr His Ser Asn Ile Trp Asp Asp Asp Phe Ile Gln
 65 70 75 80

Ser Leu Ser Thr His Tyr Gly Glu Pro Ser Tyr Gln Glu Arg Ala Glu
 85 90 95

Arg Leu Ile Val Glu Val Lys Lys Ile Phe Asn Ser Met Tyr Leu Asp
 100 105 110

Asp Gly Arg Leu Met Ser Ser Phe Asn Asp Leu Met Gln Arg Leu Trp
 115 120 125

Ile Val Asp Ser Val Glu Arg Leu Gly Ile Ala Arg His Phe Lys Asn
 130 135 140

Glu Ile Thr Ser Ala Leu Asp Tyr Val Phe Arg Tyr Trp Glu Glu Asn
 145 150 155 160

Gly Ile Gly Cys Gly Arg Asp Ser Ile Val Thr Asp Leu Asn Ser Thr
165 170 175

Ala Leu Gly Phe Arg Thr Leu Arg Leu His Gly Tyr Thr Val Ser Pro
180 185 190

Glu Val Leu Lys Ala Phe Gln Asp Gln Asn Gly Gln Phe Val Cys Ser
195 200 205

Pro Gly Gln Thr Glu Gly Glu Ile Arg Ser Val Leu Asn Leu Tyr Arg
210 215 220

Ala Ser Leu Ile Ala Phe Pro Gly Glu Lys Val Met Glu Glu Ala Glu
225 230 235 240

Ile Phe Ser Thr Arg Tyr Leu Lys Glu Ala Leu Gln Lys Ile Pro Val
245 250 255

Ser Ala Leu Ser Gln Glu Ile Lys Phe Val Met Glu Tyr Gly Trp His
260 265 270

Thr Asn Leu Pro Arg Leu Glu Ala Arg Asn Tyr Ile Asp Thr Leu Glu
275 280 285

Lys Asp Thr Ser Ala Trp Leu Asn Lys Asn Ala Gly Lys Lys Leu Leu
290 295 300

Glu Leu Ala Lys Leu Glu Phe Asn Ile Phe Asn Ser Leu Gln Gln Lys
305 310 315 320

Glu Leu Gln Tyr Leu Leu Arg Trp Trp Lys Glu Ser Asp Leu Pro Lys
325 330 335

Leu Thr Phe Ala Arg His Arg His Val Glu Phe Tyr Thr Leu Ala Ser
340 345 350

Cys Ile Ala Ile Asp Pro Lys His Ser Ala Phe Arg Leu Gly Phe Ala
355 360 365

Lys Met Cys His Leu Val Thr Val Leu Asp Asp Ile Tyr Asp Thr Phe
370 375 380

Gly Thr Ile Asp Glu Leu Glu Leu Phe Thr Ser Ala Ile Lys Arg Trp
385 390 395 400

Asn Ser Ser Glu Ile Glu His Leu Pro Glu Tyr Met Lys Cys Val Tyr

405

410

415

Met Val Val Phe Glu Thr Val Asn Glu Leu Thr Arg Glu Ala Glu Lys
 420 425 430

Thr Gln Gly Arg Asn Thr Leu Asn Tyr Val Arg Lys Ala Trp Glu Ala
 435 440 445

Tyr Phe Asp Ser Tyr Met Glu Glu Ala Lys Trp Ile Ser Asn Gly Tyr
 450 455 460

Leu Pro Thr Phe Glu Glu Tyr His Glu Asn Gly Lys Val Ser Ser Ala
 465 470 475 480

Tyr Arg Val Ala Thr Leu Gln Pro Ile Leu Thr Leu Asn Ala Trp Leu
 485 490 495

Pro Asp Tyr Ile Leu Lys Gly Ile Asp Phe Pro Ser Arg Phe Asn Asp
 500 505 510

Leu Ala Ser Ser Phe Leu Arg Leu Arg Gly Asp Thr Arg Cys Tyr Lys
 515 520 525

Ala Asp Arg Asp Arg Gly Glu Glu Ala Ser Cys Ile Ser Cys Tyr Met
 530 535 540

Lys Asp Asn Pro Gly Ser Thr Glu Glu Asp Ala Leu Asn His Ile Asn
 545 550 555 560

Ala Met Val Asn Asp Ile Ile Lys Glu Leu Asn Trp Glu Leu Leu Arg
 565 570 575

Ser Asn Asp Asn Ile Pro Met Leu Ala Lys Lys His Ala Phe Asp Ile
 580 585 590

Thr Arg Ala Leu His His Leu Tyr Ile Tyr Arg Asp Gly Phe Ser Val
 595 600 605

Ala Asn Lys Glu Thr Lys Lys Leu Val Met Glu Thr Leu Leu Glu Ser
 610 615 620

Met Leu Phe
 625

<210> 33

<211> 24

<212> DNA
<213> Artificial Sequence

<220>
<223> PCR Oligonucleotide Primer 2.2 BamHI

<400> 33
caaagggatc cagaatggct ctgg

24

<210> 34
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> PCR Oligonucleotide Primer 2.2 Not I

<400> 34
agtaagcggc cgcttttttaa tcataccac

30

<210> 35
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> PCR Oligonucleotide Primer 3.18 EcoRI

<400> 35
ctgcaggaat tcggcacgag c

21

<210> 36
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> PCR Oligonucleotide Primer3.18 SmaI

<400> 36
catagccccg ggcatagatt tgagctg

27

<210> 37
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> PCR Oligonucleotide Primer 10 NdeI

<400> 37
ggcaggaaca tatggctctc ctttctatcg

30

<210> 38
<211> 30
<212> DNA

gtcctcacat ggtaatatgt gagttgtgaa attctcaaaa aaaaaaaaaa aaaaaaaaaa 2103
 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 2163
 aaaaaaaaaa aaaaaaaaaa aaa 2186

<210> 67
 <211> 630
 <212> PRT
 <213> Abies Grandis

<400> 67

Met Ala Leu Val Ser Ser Ala Pro Lys Ser Cys Leu His Lys Ser Leu
 1 5 10 15

Ile Arg Ser Thr His His Glu Leu Lys Pro Leu Arg Arg Thr Ile Pro
 20 25 30

Thr Leu Gly Met Cys Arg Arg Gly Lys Ser Phe Thr Pro Ser Val Ser
 35 40 45

Met Ser Leu Thr Thr Ala Val Ser Asp Asp Gly Leu Gln Arg Arg Ile
 50 55 60

Gly Asp Tyr His Ser Asn Leu Trp Asp Asp Asp Phe Ile Gln Ser Leu
 65 70 75 80

Ser Thr Pro Tyr Gly Glu Pro Ser Tyr Arg Glu Arg Ala Glu Lys Leu
 85 90 95

Ile Gly Glu Val Lys Glu Met Phe Asn Ser Met Pro Ser Glu Asp Gly
 100 105 110

Glu Ser Met Ser Pro Leu Asn Asp Leu Ile Glu Arg Leu Trp Met Val
 115 120 125

Asp Ser Val Glu Arg Leu Gly Ile Asp Arg His Phe Lys Lys Glu Ile
 130 135 140

Lys Ser Ala Leu Asp Tyr Val Tyr Ser Tyr Trp Asn Glu Lys Gly Ile
 145 150 155 160

Gly Cys Gly Arg Asp Ser Val Phe Pro Asp Val Asn Ser Thr Ala Ser
 165 170 175

Gly Phe Arg Thr Leu Arg Leu His Gly Tyr Ser Val Ser Ser Glu Val
 180 185 190

Leu Lys Val Phe Gln Asp Gln Asn Gly Gln Phe Ala Phe Ser Pro Ser
195 200 205

Thr Lys Glu Arg Asp Ile Arg Thr Val Leu Asn Leu Tyr Arg Ala Ser
210 215 220

Phe Ile Ala Phe Pro Gly Glu Lys Val Met Glu Glu Ala Glu Ile Phe
225 230 235 240

Ser Ser Arg Tyr Leu Lys Glu Ala Val Gln Lys Ile Pro Val Ser Ser
245 250 255

Leu Ser Gln Glu Ile Asp Tyr Thr Leu Glu Tyr Gly Trp His Thr Asn
260 265 270

Met Pro Arg Leu Glu Thr Arg Asn Tyr Leu Asp Val Phe Gly His Pro
275 280 285

Thr Ser Pro Trp Leu Lys Lys Lys Arg Thr Gln Tyr Leu Asp Ser Glu
290 295 300

Lys Leu Leu Glu Leu Ala Lys Leu Glu Phe Asn Ile Phe His Ser Leu
305 310 315 320

Gln Gln Lys Glu Leu Gln Tyr Leu Ser Arg Trp Trp Ile His Ser Gly
325 330 335

Leu Pro Glu Leu Thr Phe Gly Arg His Arg His Val Glu Tyr Tyr Thr
340 345 350

Leu Ser Ser Cys Ile Ala Thr Glu Pro Lys His Ser Ala Phe Arg Leu
355 360 365

Gly Phe Ala Lys Thr Cys His Leu Ile Thr Val Leu Asp Asp Ile Tyr
370 375 380

Asp Thr Phe Gly Thr Met Asp Glu Ile Glu Leu Phe Asn Glu Ala Val
385 390 395 400

Arg Arg Trp Asn Pro Ser Glu Lys Glu Arg Leu Pro Glu Tyr Met Lys
405 410 415

Glu Ile Tyr Met Ala Leu Tyr Glu Ala Leu Thr Asp Met Ala Arg Glu
420 425 430

Ala Glu Lys Thr Gln Gly Arg Asp Thr Leu Asn Tyr Ala Arg Lys Ala
435 440 445

Trp Glu Val Tyr Leu Asp Ser Tyr Thr Gln Glu Ala Lys Trp Ile Ala
450 455 460

Ser Gly Tyr Leu Pro Thr Phe Glu Glu Tyr Leu Glu Asn Ala Lys Val
465 470 475 480

Ser Ser Gly His Arg Ala Ala Ala Leu Thr Pro Leu Leu Thr Leu Asp
485 490 495

Val.Pro Leu Pro Asp Asp Val Leu Lys Gly Ile Asp Phe Pro Ser Arg
500 505 510

Phe Asn Asp Leu Ala Ser Ser Phe Leu Arg Leu Arg Gly Asp Thr Arg
515 520 525

Cys Tyr Lys Ala Asp Arg Asp Arg Gly Glu Glu Ala Ser Ser Ile Ser
530 535 540

Cys Tyr Met Lys Asp Asn Pro Gly Leu Thr Glu Glu Asp Ala Leu Asn
545 550 555 560

His Ile Asn Ala Met Ile Asn Asp Ile Ile Lys Glu Leu Asn Trp Glu
565 570 575

Leu Leu Lys Pro Asp Ser Asn Ile Pro Met Thr Ala Arg Lys His Ala
580 585 590

Tyr Glu Ile Thr Arg Ala Phe His Gln Leu Tyr Lys Tyr Arg Asp Gly
595 600 605

Phe Ser Val Ala Thr Gln Glu Thr Lys Ser Leu Val Arg Arg Thr Val
610 615 620

Leu Glu Pro Val Pro Leu
625 630

<210> 68
<211> 2429
<212> DNA
<213> Abies Grandis

<220>
<221> CDS
<222> (35)..(1945)
<223>

<400> 68

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tct ttg cag gtt ccc aaa tcc tgc ggg ctg aaa tcg ttg atc agt tcc	103
Ser Leu Gln Val Pro Lys Ser Cys Gly Leu Lys Ser Leu Ile Ser Ser	
10 15 20	
agc aat gtg cag aag gct ctc tgt atc tct aca gca gtc cca act ctc	151
Ser Asn Val Gln Lys Ala Leu Cys Ile Ser Thr Ala Val Pro Thr Leu	
25 30 35	
aga atg cgt agg cga cag aaa gct ctg gtc atc aac atg aaa ttg acc	199
Arg Met Arg Arg Arg Gln Lys Ala Leu Val Ile Asn Met Lys Leu Thr	
40 45 50 55	
act gta tcc cat cgt gat gat aat ggt ggt ggt gta ctg caa aga cgc	247
Thr Val Ser His Arg Asp Asp Asn Gly Gly Gly Val Leu Gln Arg Arg	
60 65 70	
ata gcc gat cat cat ccc aac ctg tgg gaa gat gat ttc ata caa tca	295
Ile Ala Asp His His Pro Asn Leu Trp Glu Asp Asp Phe Ile Gln Ser	
75 80 85	
ttg tcc tca cct tat ggg gga tct tcg tac agt gaa cgt gct gtg aca	343
Leu Ser Ser Pro Tyr Gly Gly Ser Ser Tyr Ser Glu Arg Ala Val Thr	
90 95 100	
gtg gtt gag gaa gta aaa gag atg ttc aat tca ata cca aat aat aga	391
Val Val Glu Glu Val Lys Glu Met Phe Asn Ser Ile Pro Asn Asn Arg	
105 110 115	
gaa tta ttt ggt tcc caa aat gat ctc ctt aca cgc ctt tgg atg gtg	439
Glu Leu Phe Gly Ser Gln Asn Asp Leu Leu Thr Arg Leu Trp Met Val	
120 125 130 135	
gat agc att gaa cgt ctg ggg ata gat aga cat ttc caa aat gag ata	487
Asp Ser Ile Glu Arg Leu Gly Ile Asp Arg His Phe Gln Asn Glu Ile	
140 145 150	
aga gta gcc ctc gat tat gtt tac agt tat tgg aag gaa aag gaa ggc	535
Arg Val Ala Leu Asp Tyr Val Tyr Ser Tyr Trp Lys Glu Lys Glu Gly	
155 160 165	
att ggg tgt ggc aga gat tct act ttt cct gat ctc aac tcg act gct	583
Ile Gly Cys Gly Arg Asp Ser Thr Phe Pro Asp Leu Asn Ser Thr Ala	
170 175 180	
ctg gcg ctt cga act ctt cga ctg cac gga tac aat gtg tct tca gat	631
Leu Ala Leu Arg Thr Leu Arg Leu His Gly Tyr Asn Val Ser Ser Asp	
185 190 195	
gtg ctg gaa tac ttc aaa gat caa aag ggg cat ttt gcc tgc cct gca	679
Val Leu Glu Tyr Phe Lys Asp Gln Lys Gly His Phe Ala Cys Pro Ala	
200 205 210 215	
atc cta acc gag gga cag atc act aga agt gtt cta aat tta tat cgg	727
Ile Leu Thr Glu Gly Gln Ile Thr Arg Ser Val Leu Asn Leu Tyr Arg	

220						225						230						
gct	tcc	ctg	gtc	gcc	ttt	ccg	ggg	gag	aaa	gtt	atg	gaa	gag	gct	gaa	775		
Ala	Ser	Leu	Val	Ala	Phe	Pro	Gly	Glu	Lys	Val	Met	Glu	Glu	Ala	Glu			
			235					240					245					
atc	ttc	tcg	gca	tct	tat	ttg	aaa	gaa	gtc	tta	caa	aag	att	cca	gtc	823		
Ile	Phe	Ser	Ala	Ser	Tyr	Leu	Lys	Glu	Val	Leu	Gln	Lys	Ile	Pro	Val			
		250					255					260						
tcc	agt	ttt	tca	cga	gag	ata	gaa	tac	gtt	ttg	gaa	tat	ggt	tgg	cac	871		
Ser	Ser	Phe	Ser	Arg	Glu	Ile	Glu	Tyr	Val	Leu	Glu	Tyr	Gly	Trp	His			
	265					270					275							
aca	aat	ttg	cca	aga	ttg	gaa	gca	aga	aat	tat	atc	gac	gtc	tac	ggg	919		
Thr	Asn	Leu	Pro	Arg	Leu	Glu	Ala	Arg	Asn	Tyr	Ile	Asp	Val	Tyr	Gly			
280					285					290					295			
cag	gac	agc	tat	gaa	agt	tca	aac	gag	atg	cca	tat	gtg	aat	acg	cag	967		
Gln	Asp	Ser	Tyr	Glu	Ser	Ser	Asn	Glu	Met	Pro	Tyr	Val	Asn	Thr	Gln			
				300					305					310				
aag	ctt	tta	aaa	ctt	gca	aaa	ttg	gag	ttt	aat	atc	ttt	cac	tct	ttg	1015		
Lys	Leu	Leu	Lys	Leu	Ala	Lys	Leu	Glu	Phe	Asn	Ile	Phe	His	Ser	Leu			
			315					320					325					
caa	cag	aaa	gag	ttg	caa	tat	atc	tct	aga	tgg	tgg	aaa	gat	tcg	tgt	1063		
Gln	Gln	Lys	Glu	Leu	Gln	Tyr	Ile	Ser	Arg	Trp	Trp	Lys	Asp	Ser	Cys			
		330					335					340						
tca	tct	cat	ctg	act	ttt	act	cga	cac	cgt	cac	gtg	gaa	tac	tac	aca	1111		
Ser	Ser	His	Leu	Thr	Phe	Thr	Arg	His	Arg	His	Val	Glu	Tyr	Tyr	Thr			
	345					350					355							
atg	gca	tct	tgc	att	tct	atg	gag	ccg	aaa	cac	tcc	gct	ttc	aga	ttg	1159		
Met	Ala	Ser	Cys	Ile	Ser	Met	Glu	Pro	Lys	His	Ser	Ala	Phe	Arg	Leu			
360					365					370					375			
ggg	ttt	gtc	aaa	aca	tgt	cat	ctt	cta	aca	gtt	ctg	gat	gat	atg	tat	1207		
Gly	Phe	Val	Lys	Thr	Cys	His	Leu	Leu	Thr	Val	Leu	Asp	Asp	Met	Tyr			
				380				385						390				
gac	act	ttt	gga	aca	ctg	gac	gaa	ctc	caa	ctt	ttt	acg	act	gcc	ttt	1255		
Asp	Thr	Phe	Gly	Thr	Leu	Asp	Glu	Leu	Gln	Leu	Phe	Thr	Thr	Ala	Phe			
			395					400					405					
aag	aga	tgg	gat	ttg	tca	gag	aca	aag	tgt	ctt	cca	gaa	tat	atg	aaa	1303		
Lys	Arg	Trp	Asp	Leu	Ser	Glu	Thr	Lys	Cys	Leu	Pro	Glu	Tyr	Met	Lys			
		410					415					420						
gca	gtg	tac	atg	gac	ttg	tat	caa	tgt	ctt	aat	gaa	ttg	gcg	caa	gag	1351		
Ala	Val	Tyr	Met	Asp	Leu	Tyr	Gln	Cys	Leu	Asn	Glu	Leu	Ala	Gln	Glu			
	425					430					435							
gct	gag	aag	act	caa	ggc	aga	gat	acg	ctc	aac	tat	att	cgc	aat	gct	1399		
Ala	Glu	Lys	Thr	Gln	Gly	Arg	Asp	Thr	Leu	Asn	Tyr	Ile	Arg	Asn	Ala			
440					445					450					455			
tat	gag	tct	cat	ttt	gat	tcg	ttt	atg	cac	gaa	gca	aaa	tgg	atc	tca	1447		
Tyr	Glu	Ser	His	Phe	Asp	Ser	Phe	Met	His	Glu	Ala	Lys	Trp	Ile	Ser			
				460				465						470				

agt ggt tat ctc cca acg ttt gag gag tac ttg aag aat ggg aaa gtt	1495
Ser Gly Tyr Leu Pro Thr Phe Glu Glu Tyr Leu Lys Asn Gly Lys Val	
475 480 485	
agt tcc ggt tct cgc aca gcc act tta caa ccc ata ctc acc ttg gat	1543
Ser Ser Gly Ser Arg Thr Ala Thr Leu Gln Pro Ile Leu Thr Leu Asp	
490 495 500	
gta cca ctt cct aat tac ata ctg caa gaa att gat tat cca tct agg	1591
Val Pro Leu Pro Asn Tyr Ile Leu Gln Glu Ile Asp Tyr Pro Ser Arg	
505 510 515	
ttc aat gac ttg gct tcg tcc ctc ctt cgg cta cgt ggt gac acg cgc	1639
Phe Asn Asp Leu Ala Ser Ser Leu Leu Arg Leu Arg Gly Asp Thr Arg	
520 525 530 535	
tgc tac aag gcg gat agg gct cgt gga gaa gaa gct tca gct ata tcg	1687
Cys Tyr Lys Ala Asp Arg Ala Arg Gly Glu Glu Ala Ser Ala Ile Ser	
540 545 550	
tgt tat atg aaa gac cat cct gga tca aca gag gaa gat gct ctc aat	1735
Cys Tyr Met Lys Asp His Pro Gly Ser Thr Glu Glu Asp Ala Leu Asn	
555 560 565	
cat atc aac gtc atg atc agt gat gca atc aga gaa tta aat tgg gag	1783
His Ile Asn Val Met Ile Ser Asp Ala Ile Arg Glu Leu Asn Trp Glu	
570 575 580	
ctt ctc aga cca gat agc aaa agt ccc atc tct tcc aag aaa cat gct	1831
Leu Leu Arg Pro Asp Ser Lys Ser Pro Ile Ser Ser Lys Lys His Ala	
585 590 595	
ttt gac atc acc aga gct ttc cat cac ctc tac aag tac cga gat ggt	1879
Phe Asp Ile Thr Arg Ala Phe His His Leu Tyr Lys Tyr Arg Asp Gly	
600 605 610 615	
tac act gtt gcg agt agt gaa aca aag aat ttg gtg atg aaa aca gtt	1927
Tyr Thr Val Ala Ser Ser Glu Thr Lys Asn Leu Val Met Lys Thr Val	
620 625 630	
ctt gaa cct gtg gca ttg taaaaaata tcaaccgcat caaaatgcac	1975
Leu Glu Pro Val Ala Leu	
635	
ggagtttgta atttaatgca cttctcttat aatacacttc tcttttagacc tgtagtgaag	2035
ccgatgcacc attacagtgt atatgggagc cagtctagtc tcaaaaagtt tgtaaatggt	2095
attctatgat atactcttta gaccaaagc tagatgccca tgaaaagcaa gtgtttttaga	2155
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cttcactgcc atataagata acgggagtga caaggatttt aaagaggatt tttttttatg	2275
tcccgcata caaggtttgt cgatttacag ttgttttcaa gactgaagta ggatttccac	2335
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<210> 69
<211> 637
<212> PRT
<213> Abies Grandis

<400> 69

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20 25 30

Ser Thr Ala Val Pro Thr Leu Arg Met Arg Arg Arg Gln Lys Ala Leu
35 40 45

Val Ile Asn Met Lys Leu Thr Thr Val Ser His Arg Asp Asp Asn Gly
50 55 60

Gly Gly Val Leu Gln Arg Arg Ile Ala Asp His His Pro Asn Leu Trp
65 70 75 80

Glu Asp Asp Phe Ile Gln Ser Leu Ser Ser Pro Tyr Gly Gly Ser Ser
85 90 95

Tyr Ser Glu Arg Ala Val Thr Val Val Glu Glu Val Lys Glu Met Phe
100 105 110

Asn Ser Ile Pro Asn Asn Arg Glu Leu Phe Gly Ser Gln Asn Asp Leu
115 120 125

Leu Thr Arg Leu Trp Met Val Asp Ser Ile Glu Arg Leu Gly Ile Asp
130 135 140

Arg His Phe Gln Asn Glu Ile Arg Val Ala Leu Asp Tyr Val Tyr Ser
145 150 155 160

Tyr Trp Lys Glu Lys Glu Gly Ile Gly Cys Gly Arg Asp Ser Thr Phe
165 170 175

Pro Asp Leu Asn Ser Thr Ala Leu Ala Leu Arg Thr Leu Arg Leu His
180 185 190

Gly Tyr Asn Val Ser Ser Asp Val Leu Glu Tyr Phe Lys Asp Gln Lys
195 200 205

Gly His Phe Ala Cys Pro Ala Ile Leu Thr Glu Gly Gln Ile Thr Arg

210

215

220

Ser Val Leu Asn Leu Tyr Arg Ala Ser Leu Val Ala Phe Pro Gly Glu
 225 230 235 240

Lys Val Met Glu Glu Ala Glu Ile Phe Ser Ala Ser Tyr Leu Lys Glu
 245 250 255

Val Leu Gln Lys Ile Pro Val Ser Ser Phe Ser Arg Glu Ile Glu Tyr
 260 265 270

Val Leu Glu Tyr Gly Trp His Thr Asn Leu Pro Arg Leu Glu Ala Arg
 275 280 285

Asn Tyr Ile Asp Val Tyr Gly Gln Asp Ser Tyr Glu Ser Ser Asn Glu
 290 295 300

Met Pro Tyr Val Asn Thr Gln Lys Leu Leu Lys Leu Ala Lys Leu Glu
 305 310 315 320

Phe Asn Ile Phe His Ser Leu Gln Gln Lys Glu Leu Gln Tyr Ile Ser
 325 330 335

Arg Trp Trp Lys Asp Ser Cys Ser Ser His Leu Thr Phe Thr Arg His
 340 345 350

Arg His Val Glu Tyr Tyr Thr Met Ala Ser Cys Ile Ser Met Glu Pro
 355 360 365

Lys His Ser Ala Phe Arg Leu Gly Phe Val Lys Thr Cys His Leu Leu
 370 375 380

Thr Val Leu Asp Asp Met Tyr Asp Thr Phe Gly Thr Leu Asp Glu Leu
 385 390 395 400

Gln Leu Phe Thr Thr Ala Phe Lys Arg Trp Asp Leu Ser Glu Thr Lys
 405 410 415

Cys Leu Pro Glu Tyr Met Lys Ala Val Tyr Met Asp Leu Tyr Gln Cys
 420 425 430

Leu Asn Glu Leu Ala Gln Glu Ala Glu Lys Thr Gln Gly Arg Asp Thr
 435 440 445

Leu Asn Tyr Ile Arg Asn Ala Tyr Glu Ser His Phe Asp Ser Phe Met
 450 455 460

His Glu Ala Lys Trp Ile Ser Ser Gly Tyr Leu Pro Thr Phe Glu Glu
465 470 475 480

Tyr Leu Lys Asn Gly Lys Val Ser Ser Gly Ser Arg Thr Ala Thr Leu
485 490 495

Gln Pro Ile Leu Thr Leu Asp Val Pro Leu Pro Asn Tyr Ile Leu Gln
500 505 510

Glu Ile Asp Tyr Pro Ser Arg Phe Asn Asp Leu Ala Ser Ser Leu Leu
515 520 525

Arg Leu Arg Gly Asp Thr Arg Cys Tyr Lys Ala Asp Arg Ala Arg Gly
530 535 540

Glu Glu Ala Ser Ala Ile Ser Cys Tyr Met Lys Asp His Pro Gly Ser
545 550 555 560

Thr Glu Glu Asp Ala Leu Asn His Ile Asn Val Met Ile Ser Asp Ala
565 570 575

Ile Arg Glu Leu Asn Trp Glu Leu Leu Arg Pro Asp Ser Lys Ser Pro
580 585 590

Ile Ser Ser Lys Lys His Ala Phe Asp Ile Thr Arg Ala Phe His His
595 600 605

Leu Tyr Lys Tyr Arg Asp Gly Tyr Thr Val Ala Ser Ser Glu Thr Lys
610 615 620

Asn Leu Val Met Lys Thr Val Leu Glu Pro Val Ala Leu
625 630 635

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<212> DNA

<213> Abies grandis

<400> 70

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cgagagacgc tcaacgatgc tcgacgagct tgggaggcct atcttgattc gtatatgaaa	180
gaagctgagt ggatctccag tggttatctg ccaacgtttg aggagtacat ggagaccagc	240
aaagttagtt ttggttatcg catattcgca ttgcaaccca tcctcactat ggatgttccc	300

cttactcacc acatcctgca ggaaatagac tttccattga ggtttaatga cttaatatgt	360
tccatccttc gacttaaaaa tgacactcgc tgctacaagg cggacagggc ccgtggagaa	420
gaagcttcgt gtatatcgtg ttatatgaaa gagaatcctg gatcaacaga ggaagatgct	480
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cgacaggacg gcaccgctca tattgcttgc aagaaacacg cttttgacat cctcaaaggt	600
tcccttcacg gctacaaata ccgagatggg ttcagcgttg ccaacaagga aaccaagaat	660
tgggtgagga gaacagtcct tgagtctgtg cctttg	696

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<210> 73
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<400> 73	
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<210> 74
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<400> 74

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23

<210> 75
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<400> 75
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24

<210> 76
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<212> DNA
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<223> Oligonucleotide PCR Primer AG9R

<400> 76
ttacaaaggc acagactcaa ggac

24

<210> 77
<211> 1890
<212> DNA
<213> Abies Grandis

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<222> (1)..(1890)
<223>

<400> 77
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Met Ala Leu Val Ser Ile Leu Pro Leu Ser Ser Lys Ser Val Leu His
1 5 10 15

48

aaa tcg tgg atc gtt tct act tat gag cat aag gct atc agt aga aca
Lys Ser Trp Ile Val Ser Thr Tyr Glu His Lys Ala Ile Ser Arg Thr
20 25 30

96

atc cca aat ctt gga ttg cgt ggg cga ggg aaa tct gtg aca cat tcc
Ile Pro Asn Leu Gly Leu Arg Gly Arg Gly Lys Ser Val Thr His Ser
35 40 45

144

ctg aga atg agt ttg agc acc gca gtc tct gat gat cat ggt gta caa
Leu Arg Met Ser Leu Ser Thr Ala Val Ser Asp Asp His Gly Val Gln
50 55 60

192

aga cgc ata gtc gag ttt cat tcc aat ctg tgg gac gac gat ttc ata
Arg Arg Ile Val Glu Phe His Ser Asn Leu Trp Asp Asp Asp Phe Ile
65 70 75 80

240

caa tct cta tca acg cct tat ggg gca cct tca tac cgt gaa cgt gct
Gln Ser Leu Ser Thr Pro Tyr Gly Ala Pro Ser Tyr Arg Glu Arg Ala

288

				85					90					95					
gat	aga	ctt	att	gtg	gaa	gta	aag	ggg	ata	ttc	act	tca	att	tca	gcg		336		
Asp	Arg	Leu	Ile	Val	Glu	Val	Lys	Gly	Ile	Phe	Thr	Ser	Ile	Ser	Ala				
				100					105					110					
gaa	gat	gga	gaa	cta	atc	act	ccc	ctc	aat	gat	ctc	att	caa	cgc	ctt		384		
Glu	Asp	Gly	Glu	Leu	Ile	Thr	Pro	Leu	Asn	Asp	Leu	Ile	Gln	Arg	Leu				
				115					120					125					
tta	atg	gtc	gat	aac	gtt	gaa	cgt	tta	ggg	att	gat	aga	cat	ttc	aaa		432		
Leu	Met	Val	Asp	Asn	Val	Glu	Arg	Leu	Gly	Ile	Asp	Arg	His	Phe	Lys				
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aat	gag	ata	aaa	gca	gca	cta	gac	tat	gtt	tac	agt	tat	tgg	aac	gaa		480		
Asn	Glu	Ile	Lys	Ala	Ala	Leu	Asp	Tyr	Val	Tyr	Ser	Tyr	Trp	Asn	Glu				
				145					150					155					
aaa	ggc	att	ggc	agt	gga	agt	gat	agt	ggg	gtt	gct	gat	ctc	aac	tca		528		
Lys	Gly	Ile	Gly	Ser	Gly	Ser	Asp	Ser	Gly	Val	Ala	Asp	Leu	Asn	Ser				
				165					170					175					
act	gcc	ctg	ggg	ttt	cga	att	ctt	cga	cta	cac	gga	tac	agt	gtt	tct		576		
Thr	Ala	Leu	Gly	Phe	Arg	Ile	Leu	Arg	Leu	His	Gly	Tyr	Ser	Val	Ser				
				180					185					190					
tca	gat	gtg	ttg	gaa	cac	ttc	aaa	gag	gag	aag	gag	aag	ggg	cag	ttt		624		
Ser	Asp	Val	Leu	Glu	His	Phe	Lys	Glu	Glu	Lys	Glu	Lys	Gly	Gln	Phe				
				195					200					205					
gta	tgt	tcg	gcc	atc	caa	aca	gag	gaa	gag	ata	aaa	agc	gtt	ctg	aat		672		
Val	Cys	Ser	Ala	Ile	Gln	Thr	Glu	Glu	Glu	Ile	Lys	Ser	Val	Leu	Asn				
				210					215					220					
tta	ttt	cgg	gcc	tcc	ctc	att	gcc	ttt	cct	ggg	gag	aaa	gtt	atg	gaa		720		
Leu	Phe	Arg	Ala	Ser	Leu	Ile	Ala	Phe	Pro	Gly	Glu	Lys	Val	Met	Glu				
				225					230					235					
gag	gct	gaa	atc	ttc	tct	aaa	ata	tat	tta	aaa	gaa	gcc	tta	caa	aat		768		
Glu	Ala	Glu	Ile	Phe	Ser	Lys	Ile	Tyr	Leu	Lys	Glu	Ala	Leu	Gln	Asn				
				245					250					255					
att	gct	gtc	tcc	agt	ctt	tca	cga	gag	ata	gag	tac	gtt	ctg	gag	gat		816		
Ile	Ala	Val	Ser	Ser	Leu	Ser	Arg	Glu	Ile	Glu	Tyr	Val	Leu	Glu	Asp				
				260					265					270					
ggg	tgg	caa	aca	aat	atg	cca	aga	ttg	gaa	aca	agg	aac	tac	atc	gat		864		
Gly	Trp	Gln	Thr	Asn	Met	Pro	Arg	Leu	Glu	Thr	Arg	Asn	Tyr	Ile	Asp				
				275					280					285					
gta	ttg	gga	gag	aac	gat	cgt	gat	gag	acg	tta	tat	atg	aac	atg	gag		912		
Val	Leu	Gly	Glu	Asn	Asp	Arg	Asp	Glu	Thr	Leu	Tyr	Met	Asn	Met	Glu				
				290					295					300					
aaa	ctt	tta	gaa	att	gca	aaa	ttg	gag	ttc	aat	att	ttt	cac	tcc	tta		960		
Lys	Leu	Leu	Glu	Ile	Ala	Lys	Leu	Glu	Phe	Asn	Ile	Phe	His	Ser	Leu				
				305					310					315					
caa																			

ttc tct cac ctg aca ttt tct cgg cat cgt cat gtg gaa ttc tac gct Phe Ser His Leu Thr Phe Ser Arg His Arg His Val Glu Phe Tyr Ala 340 345 350	1056
ctg gca tct tgc att gaa act gat cgc aaa cat tcc gga ttc aga ctc Leu Ala Ser Cys Ile Glu Thr Asp Arg Lys His Ser Gly Phe Arg Leu 355 360 365	1104
ggc ttt gcc aaa atg tgt cat ctt atc acg gtt ttg gac gat ata tac Gly Phe Ala Lys Met Cys His Leu Ile Thr Val Leu Asp Asp Ile Tyr 370 375 380	1152
gac acc ttt gga aca atg gag gag ctg gaa ctc ttc act gca gca ttt Asp Thr Phe Gly Thr Met Glu Glu Leu Glu Leu Phe Thr Ala Ala Phe 385 390 395 400	1200
aag aga tgg gat ccg tct gcc aca gat ttg ctt cca gag tat atg aaa Lys Arg Trp Asp Pro Ser Ala Thr Asp Leu Leu Pro Glu Tyr Met Lys 405 410 415	1248
ggg ttg tac atg gtg gtt tac gaa acc gta aat gaa att gct cga gag Gly Leu Tyr Met Val Val Tyr Glu Thr Val Asn Glu Ile Ala Arg Glu 420 425 430	1296
gca gac aag tct caa ggc cga gag acg ctc aac gat gct cga cga gct Ala Asp Lys Ser Gln Gly Arg Glu Thr Leu Asn Asp Ala Arg Arg Ala 435 440 445	1344
tgg gag gcc tat ctt gat tcg tat atg aaa gaa gct gag tgg atc tcc Trp Glu Ala Tyr Leu Asp Ser Tyr Met Lys Glu Ala Glu Trp Ile Ser 450 455 460	1392
agt ggt tat ctg cca acg ttt gag gag tac atg gag acc agc aaa gtt Ser Gly Tyr Leu Pro Thr Phe Glu Glu Tyr Met Glu Thr Ser Lys Val 465 470 475 480	1440
agt ttt ggt tat cgc ata ttc gca ttg caa ccc atc ctc act atg gat Ser Phe Gly Tyr Arg Ile Phe Ala Leu Gln Pro Ile Leu Thr Met Asp 485 490 495	1488
gtt ccc ctt act cac cac atc ctg cag gaa ata gac ttt cca ttg agg Val Pro Leu Thr His His Ile Leu Gln Glu Ile Asp Phe Pro Leu Arg 500 505 510	1536
ttt aat gac tta ata tgt tcc atc ctt cga ctt aaa aat gac act cgc Phe Asn Asp Leu Ile Cys Ser Ile Leu Arg Leu Lys Asn Asp Thr Arg 515 520 525	1584
tgc tac aag gcg gac agg gcc cgt gga gaa gaa gct tcg tgt ata tcg Cys Tyr Lys Ala Asp Arg Ala Arg Gly Glu Glu Ala Ser Cys Ile Ser 530 535 540	1632
tgt tat atg aaa gag aat cct gga tca aca gag gaa gat gct atc aat Cys Tyr Met Lys Glu Asn Pro Gly Ser Thr Glu Glu Asp Ala Ile Asn 545 550 555 560	1680
cat atc aac gct atg gtc aat aac tta atc aaa gaa gtg aat tgg gag His Ile Asn Ala Met Val Asn Asn Leu Ile Lys Glu Val Asn Trp Glu 565 570 575	1728

ctt ctc cga cag gac ggc acc gct cat att gct tgc aag aaa cac gct 1776
 Leu Leu Arg Gln Asp Gly Thr Ala His Ile Ala Cys Lys Lys His Ala
 580 585 590

ttt gac atc ctc aaa ggt tcc ctt cac ggc tac aaa tac cga gat ggg 1824
 Phe Asp Ile Leu Lys Gly Ser Leu His Gly Tyr Lys Tyr Arg Asp Gly
 595 600 605

ttc agc gtt gcc aac aag gaa acc aag aat tgg gtg agg aga aca gtc 1872
 Phe Ser Val Ala Asn Lys Glu Thr Lys Asn Trp Val Arg Arg Thr Val
 610 615 620

ctt gag tct gtg cct ttg 1890
 Leu Glu Ser Val Pro Leu
 625 630

<210> 78
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 <213> Abies Grandis

<400> 78

Met Ala Leu Val Ser Ile Leu Pro Leu Ser Ser Lys Ser Val Leu His
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Lys Ser Trp Ile Val Ser Thr Tyr Glu His Lys Ala Ile Ser Arg Thr
 20 25 30

Ile Pro Asn Leu Gly Leu Arg Gly Arg Gly Lys Ser Val Thr His Ser
 35 40 45

Leu Arg Met Ser Leu Ser Thr Ala Val Ser Asp Asp His Gly Val Gln
 50 55 60

Arg Arg Ile Val Glu Phe His Ser Asn Leu Trp Asp Asp Asp Phe Ile
 65 70 75 80

Gln Ser Leu Ser Thr Pro Tyr Gly Ala Pro Ser Tyr Arg Glu Arg Ala
 85 90 95

Asp Arg Leu Ile Val Glu Val Lys Gly Ile Phe Thr Ser Ile Ser Ala
 100 105 110

Glu Asp Gly Glu Leu Ile Thr Pro Leu Asn Asp Leu Ile Gln Arg Leu
 115 120 125

Leu Met Val Asp Asn Val Glu Arg Leu Gly Ile Asp Arg His Phe Lys
 130 135 140

Asn Glu Ile Lys Ala Ala Leu Asp Tyr Val Tyr Ser Tyr Trp Asn Glu

145

150

155

160

Lys Gly Ile Gly Ser Gly Ser Asp Ser Gly Val Ala Asp Leu Asn Ser
 165 170 175

Thr Ala Leu Gly Phe Arg Ile Leu Arg Leu His Gly Tyr Ser Val Ser
 180 185 190

Ser Asp Val Leu Glu His Phe Lys Glu Glu Lys Glu Lys Gly Gln Phe
 195 200 205

Val Cys Ser Ala Ile Gln Thr Glu Glu Glu Ile Lys Ser Val Leu Asn
 210 215 220

Leu Phe Arg Ala Ser Leu Ile Ala Phe Pro Gly Glu Lys Val Met Glu
 225 230 235 240

Glu Ala Glu Ile Phe Ser Lys Ile Tyr Leu Lys Glu Ala Leu Gln Asn
 245 250 255

Ile Ala Val Ser Ser Leu Ser Arg Glu Ile Glu Tyr Val Leu Glu Asp
 260 265 270

Gly Trp Gln Thr Asn Met Pro Arg Leu Glu Thr Arg Asn Tyr Ile Asp
 275 280 285

Val Leu Gly Glu Asn Asp Arg Asp Glu Thr Leu Tyr Met Asn Met Glu
 290 295 300

Lys Leu Leu Glu Ile Ala Lys Leu Glu Phe Asn Ile Phe His Ser Leu
 305 310 315 320

Gln Gln Arg Glu Leu Lys Asp Leu Ser Arg Trp Trp Lys Asp Ser Gly
 325 330 335

Phe Ser His Leu Thr Phe Ser Arg His Arg His Val Glu Phe Tyr Ala
 340 345 350

Leu Ala Ser Cys Ile Glu Thr Asp Arg Lys His Ser Gly Phe Arg Leu
 355 360 365

Gly Phe Ala Lys Met Cys His Leu Ile Thr Val Leu Asp Asp Ile Tyr
 370 375 380

Asp Thr Phe Gly Thr Met Glu Glu Leu Glu Leu Phe Thr Ala Ala Phe
 385 390 395 400

Lys Arg Trp Asp Pro Ser Ala Thr Asp Leu Leu Pro Glu Tyr Met Lys
405 410 415

Gly Leu Tyr Met Val Val Tyr Glu Thr Val Asn Glu Ile Ala Arg Glu
420 425 430

Ala Asp Lys Ser Gln Gly Arg Glu Thr Leu Asn Asp Ala Arg Arg Ala
435 440 445

Trp Glu Ala Tyr Leu Asp Ser Tyr Met Lys Glu Ala Glu Trp Ile Ser
450 455 460

Ser Gly Tyr Leu Pro Thr Phe Glu Glu Tyr Met Glu Thr Ser Lys Val
465 470 475 480

Ser Phe Gly Tyr Arg Ile Phe Ala Leu Gln Pro Ile Leu Thr Met Asp
485 490 495

Val Pro Leu Thr His His Ile Leu Gln Glu Ile Asp Phe Pro Leu Arg
500 505 510

Phe Asn Asp Leu Ile Cys Ser Ile Leu Arg Leu Lys Asn Asp Thr Arg
515 520 525

Cys Tyr Lys Ala Asp Arg Ala Arg Gly Glu Glu Ala Ser Cys Ile Ser
530 535 540

Cys Tyr Met Lys Glu Asn Pro Gly Ser Thr Glu Glu Asp Ala Ile Asn
545 550 555 560

His Ile Asn Ala Met Val Asn Asn Leu Ile Lys Glu Val Asn Trp Glu
565 570 575

Leu Leu Arg Gln Asp Gly Thr Ala His Ile Ala Cys Lys Lys His Ala
580 585 590

Phe Asp Ile Leu Lys Gly Ser Leu His Gly Tyr Lys Tyr Arg Asp Gly
595 600 605

Phe Ser Val Ala Asn Lys Glu Thr Lys Asn Trp Val Arg Arg Thr Val
610 615 620

Leu Glu Ser Val Pro Leu
625 630

<210> 79
<211> 30
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<220>
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<210> 80
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Oligonucleotide Mutagenesis Primer 6eBamHIR

<400> 80
ccatcgcgga cgggtcccat ctcttaattg 30

<210> 81
<211> 30
<212> DNA
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<400> 81
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<210> 82
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<223> Oligonucleotide Mutagenesis Primer 9eBamHIR

<400> 82
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<210> 83
<211> 25
<212> DNA
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<223> Oligonucleotide Mutagenesis Primer 732eNdeIF

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<210> 84
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<400> 86
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<210> 87
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<212> DNA
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<220>
<223> Oligonucleotide PCR Primer 6-BamHI

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cacccatagg ggatcctcag ttaatattg 29

<210> 88
<211> 30
<212> DNA
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<220>
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<400> 88
taagcgagca catatggctc tggtttcttc 30

<210> 89

<211> 29
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<220>
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gcataaacgc atagcggatc ctacaccaa

29

<210> 90
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<211> 34
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34

<210> 92
<211> 27
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27

<210> 93
<211> 31
<212> DNA
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<220>
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<400> 93
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31

<210> 94
<211> 34

<212> DNA
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 <211> 24
 <212> DNA
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 <400> 95
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<210> 98
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<210> 99
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<223> Oligonucleotide PCR Primer 3-BamHI

<400> 99

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<212> DNA

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<400> 100

cgtttgggaa tccatagaca tttc

24

<210> 101

<211> 24

<212> DNA

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<220>

<223> Oligonucleotide Mutagenesis Primer 3elBamHIR

<400> 101

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24

<210> 102

<211> 26

<212> DNA

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<223> Oligonucleotide PCR Primer 3e2BamHIF

<400> 102

gaagagatgg gacccgtcct cgatag

26

<210> 103

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> Oligonucleotide PCR Primer 2-NdeI-M

<400> 103

ctatcgagga cgggtcccat ctcttc

26

<210> 104

<211> 25

<212> DNA

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<223> Oligonucleotide Mutagenesis Primer 3e1NdeIF

<400> 104

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25

<210> 105

<211> 25

<212> DNA

<213> Artificial Sequence

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<400> 105

gctcttcaca taggacttcg tggtc

25

<210> 106

<211> 25

<212> DNA

<213> Artificial Sequence

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<223> Oligonucleotide Mutagenesis Primer 3e3NdeIF

<400> 106

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25

<210> 107

<211> 25

<212> DNA

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<223> Oligonucleotide Mutagenesis Primer 3e2NdeIR

<400> 107

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25

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<223> PCR Oligonucleotide Primer 10 BamHI

<400> 38

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<210> 39

<211> 18

<212> DNA

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18

<210> 40

<211> 20

<212> DNA

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<223> PCR Oligonucleotide Primer 2-8

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<211> 20

<212> DNA

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<223> PCR Oligonucleotide Primer 3-9

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<210> 42

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<223> PCR Oligonucleotide Primer 3-11

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<210> 43

<211> 20

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<223> PCR Oligonucleotide Primer 7-1

<400> 43

ccttacacgc ctttgatgg

20

<210> 44

<211> 20

<212> DNA

<213> Artificial Sequence

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<223> PCR Oligonucleotide Sequence 7-3

<400> 44

tctgttgatc caggatggtc

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<210> 45

<211> 5

<212> PRT

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<223> Conserved Amino Acid Motif Common to All Prenyl Transferases

<220>

<221> MISC_FEATURE

<222> (3)..(4)

<223> Wherein Xaa=any amino acid

<400> 45

Asp Asp Xaa Xaa Asp

1

5

<210> 46

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> Amino Acid Motif from which Oligonucleotide Primers can be Synthesized that Hybridize to the Monoterpene Synthases of the Present Invention

<220>

<221> MISC_FEATURE

<222> (4)..(4)

<223> Wherein Xaa=LEU or ILE or VAL

<400> 46

His Ser Asn Xaa Thr Asp Asp Asp

1

5

<210> 47
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Amino Acid Motif from which Degenerate Oligonucleotides can be Constructed that Hybridize to the Monoterpene Synthases of the Present Invention

<400> 47

Ala Leu Asp Tyr Val Tyr
1 5

<210> 48
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Amino Acid Motif from which Degenerate Oligonucleotide Sequences can be Constructed that Hybridize to the Monoterpene Synthases of the Present Invention

<400> 48

Glu Leu Ala Lys Leu Glu Phe
1 5

<210> 49
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Amino Acid Motif from which Degenerate Oligonucleotide Sequences can be Constructed that Hybridize to the Monoterpene Synthase Clones of the Present Invention

<400> 49

Arg Trp Trp Lys Glu Ser
1 5

<210> 50
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Amino Acid Motif from which Oligonucleotide Sequences can be Constructed that Hybridize to the Monoterpene Synthase Clones of the Present Invention

<220>
<221> MISC_FEATURE

<222> (1)..(1)
<223> Wherein Xaa=VAL or ILE or LEU

<400> 50

Xaa Leu Asp Asp Met Tyr Asp
1 5

<210> 51
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Amino Acid Motif from which Oligonucleotide Sequences can be Constructed that Hybridize to the Monoterpene Synthase Clones of the Present Invention

<220>
<221> MISC_FEATURE
<222> (1)..(1)
<223> Wherein Xaa=VAL or ILE or LEU

<400> 51

Xaa Leu Asp Asp Leu Tyr Asp
1 5

<210> 52
<211> 7
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<220>
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<223> Wherein Xaa=VAL or ILE or LEU

<400> 52

Xaa Leu Asp Asp Ile Tyr Asp
1 5

<210> 53
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tructed that Hybridize to the Monoterpene Synthase Clones of the
Present Invention

<220>
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<222> (6)..(6)
<223> Wherein Xaa=ASN or HIS

<400> 53

Cys Tyr Met Lys Asp Xaa Pro
1 5

<210> 54
<211> 9
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<213> Artificial Sequence

<220>
<223> Exemplary Oligonucleotide that Corresponds to Peptide Sequence Me
tMetMet

<400> 54
atgatgatg

9

<210> 55
<211> 9
<212> DNA
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<220>
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quence MetMetMet

<400> 55
tactactac

9

<210> 56
<211> 9
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<220>
<223> Exemplary Oligonucleotide that Corresponds to Peptide Sequence Me
tMetMet

<220>
<221> misc_feature
<222> (1)..(9)
<223> Wherein N=inosine

<400> 56
nacnacnac

9

<210> 57

<211> 24
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Oligonucleotide Corresponding to Amino Acid Sequence Set Forth in
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 <400> 57
 gtgtcgttgg agaccctgct gctg 24

 <210> 58
 <211> 18
 <212> DNA
 <213> Artificial Sequence

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 <400> 58
 cgggagctga tgcagatg 18

 <210> 59
 <211> 21
 <212> DNA
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 <220>
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 <400> 59
 ctcgagcggg tgcagctcaa g 21

 <210> 60
 <211> 18
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 <220>
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 Forth in SEQ ID NO:49

 <400> 60
 gccaccacct tcctctcg 18

 <210> 61
 <211> 21
 <212> DNA
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 <220>
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 Forth in SEQ ID NO:50

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gaggagctgc tgtacatgct g

21

<210> 62
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Oligonucleotide Corresponding to Conserved Amino Acid Sequence Set Forth in SEQ ID NO:51

<400> 62
gaggagctgc tggagatgct g

21

<210> 63
<211> 293
<212> DNA
<213> Abies Grandis

<400> 63
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ggttatctcc caacgtttga ggagtacttg aagaatggga aagttagttc cggttctcgc 180
acagccactt tacaacccat actcaccttg gatgtaccac ttctaatta catactgcaa 240
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<212> DNA
<213> Abies Grandis

<220>
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<222> (36)..(1889)
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<400> 64
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1 5

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Thr Pro Leu Val Ser Arg Ser Cys Leu Ser Ser Ser His Glu Ile Lys
10 15 20

gct ctc cgt aga aca atc cca act ctt gga atc tgc agg ccg ggg aaa 149
Ala Leu Arg Arg Thr Ile Pro Thr Leu Gly Ile Cys Arg Pro Gly Lys
25 30 35

tcc gtc gcg cat tcc ata aac atg tgt ttg aca agc gtc gca tct act 197
Ser Val Ala His Ser Ile Asn Met Cys Leu Thr Ser Val Ala Ser Thr
40 45 50

gat tct gta cag aga cgc gtg ggc aac tat cat tcc aac ctg tgg gac Asp Ser Val Gln Arg Arg Val Gly Asn Tyr His Ser Asn Leu Trp Asp 55 60 65 70	245
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ttc aat ttc aag tcg ctg gaa gat gga ggc aat gat ctc ctt caa cga Phe Asn Phe Lys Ser Leu Glu Asp Gly Gly Asn Asp Leu Leu Gln Arg 105 110 115	389
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aaa aaa gag ata aaa acg gca ctc gat tat gtt aac agt tat tgg aac Lys Lys Glu Ile Lys Thr Ala Leu Asp Tyr Val Asn Ser Tyr Trp Asn 135 140 145 150	485
gaa aaa ggc att gga tgt ggg agg gag agt gtt gtg act gac ctc aac Glu Lys Gly Ile Gly Cys Gly Arg Glu Ser Val Val Thr Asp Leu Asn 155 160 165	533
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Tyr	Leu	Pro	Thr	Phe	Glu	Glu	Tyr	Leu	Glu	Asn 465	Gly	Lys	Val	Ser	Ser 470	
gct	cat	cgc	cca	tgc	gca	ctg	caa	ccc	att	ctg	acg	ttg	gac	atc	ccc	1493
Ala	His	Arg	Pro	Cys 475	Ala	Leu	Gln	Pro	Ile 480	Leu	Thr	Leu	Asp	Ile	Pro 485	
ttt	cct	gat	cac	atc	ctc	aag	gaa	gtt	gac	ttc	cca	tcg	aag	ctc	aat	1541
Phe	Pro	Asp	His 490	Ile	Leu	Lys	Glu	Val 495	Asp	Phe	Pro	Ser	Lys 500	Leu	Asn	
gac	ttg	ata	tgt	atc	atc	ctt	cga	tta	aga	ggt	gat	aca	cgg	tgc	tac	1589
Asp	Leu	Ile	Cys	Ile	Ile	Leu	Arg	Leu	Arg	Gly	Asp	Thr 515	Arg	Cys	Tyr	
aag	gca	gac	agg	gcc	cgt	gga	gaa	gaa	gct	tcg	tct	ata	tca	tgt	tat	1637
Lys	Ala	Asp	Arg	Ala	Arg	Gly 525	Glu	Glu	Ala	Ser	Ser 530	Ile	Ser	Cys	Tyr	
atg	aaa	gac	aat	cct	gga	tta	acg	gaa	gaa	gat	gct	ctg	aat	cat	atc	1685
Met	Lys	Asp	Asn	Pro	Gly	Leu	Thr	Glu	Glu	Asp	Ala	Leu	Asn	His	Ile	

535	540	545	550	
aac ttc atg atc agg gac gca atc aga gaa tta aat tgg gag ctt cta				1733
Asn Phe Met Ile Arg Asp Ala Ile Arg Glu Leu Asn Trp Glu Leu Leu	555	560	565	
aag cca gac aac agt gtt ccc atc act tcc aag aaa cac gca ttt gac				1781
Lys Pro Asp Asn Ser Val Pro Ile Thr Ser Lys Lys His Ala Phe Asp	570	575	580	
ata agc aga gtt tgg cat cac ggt tac aga tac cga gat ggc tac agc				1829
Ile Ser Arg Val Trp His His Gly Tyr Arg Tyr Arg Asp Gly Tyr Ser	585	590	595	
ttt gcc aac gtt gaa aca aag agt ttg gtg atg aga acc gtc att gaa				1877
Phe Ala Asn Val Glu Thr Lys Ser Leu Val Met Arg Thr Val Ile Glu	600	605	610	
cct gtg cct ttg taacaacact tcaaactctac aatattaact gaggatgccc				1929
Pro Val Pro Leu	615			
tatgggtgta tatagggcac acaaaaataa atatggttgt gttagtaaag ctgtaattta				1989
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Met Ala Leu Leu Ser Ile Thr Pro Leu Val Ser Arg Ser Cys Leu Ser	1	5	10	15
Ser Ser His Glu Ile Lys Ala Leu Arg Arg Thr Ile Pro Thr Leu Gly	20	25	30	
Ile Cys Arg Pro Gly Lys Ser Val Ala His Ser Ile Asn Met Cys Leu	35	40	45	
Thr Ser Val Ala Ser Thr Asp Ser Val Gln Arg Arg Val Gly Asn Tyr	50	55	60	
His Ser Asn Leu Trp Asp Asp Asp Phe Ile Gln Ser Leu Ile Ser Thr	65	70	75	80
Pro Tyr Gly Ala Pro Asp Tyr Arg Glu Arg Ala Asp Arg Leu Ile Gly	85	90	95	
Glu Val Lys Asp Ile Met Phe Asn Phe Lys Ser Leu Glu Asp Gly Gly	100	105	110	

Asn Asp Leu Leu Gln Arg Leu Leu Leu Val Asp Asp Val Glu Arg Leu
115 120 125

Gly Ile Asp Arg His Phe Lys Lys Glu Ile Lys Thr Ala Leu Asp Tyr
130 135 140

Val Asn Ser Tyr Trp Asn Glu Lys Gly Ile Gly Cys Gly Arg Glu Ser
145 150 155 160

Val Val Thr Asp Leu Asn Ser Thr Ala Leu Gly Leu Arg Thr Leu Arg
165 170 175

Leu His Gly Tyr Thr Val Ser Ser Asp Val Leu Asn Val Phe Lys Asp
180 185 190

Lys Asn Gly Gln Phe Ser Ser Thr Ala Asn Ile Gln Ile Glu Gly Glu
195 200 205

Ile Arg Gly Val Leu Asn Leu Phe Arg Ala Ser Leu Val Ala Phe Pro
210 215 220

Gly Glu Lys Val Met Asp Glu Ala Glu Thr Phe Ser Thr Lys Tyr Leu
225 230 235 240

Arg Glu Ala Leu Gln Lys Ile Pro Ala Ser Ser Ile Leu Ser Leu Glu
245 250 255

Ile Arg Asp Val Leu Glu Tyr Gly Trp His Thr Asn Leu Pro Arg Leu
260 265 270

Glu Ala Arg Asn Tyr Met Asp Val Phe Gly Gln His Thr Lys Asn Lys
275 280 285

Asn Ala Ala Glu Lys Leu Leu Glu Leu Ala Lys Leu Glu Phe Asn Ile
290 295 300

Phe His Ser Leu Gln Glu Arg Glu Leu Lys His Val Ser Arg Trp Trp
305 310 315 320

Lys Asp Ser Gly Ser Pro Glu Met Thr Phe Cys Arg His Arg His Val
325 330 335

Glu Tyr Tyr Ala Leu Ala Ser Cys Ile Ala Phe Glu Pro Gln His Ser
340 345 350

Gly Phe Arg Leu Gly Phe Thr Lys Met Ser His Leu Ile Thr Val Leu
355 360 365

Asp Asp Met Tyr Asp Val Phe Gly Thr Val Asp Glu Leu Glu Leu Phe
370 375 380

Thr Ala Thr Ile Lys Arg Trp Asp Pro Ser Ala Met Glu Cys Leu Pro
385 390 395 400

Glu Tyr Met Lys Gly Val Tyr Met Met Val Tyr His Thr Val Asn Glu
405 410 415

Met Ala Arg Val Ala Glu Lys Ala Gln Gly Arg Asp Thr Leu Asn Tyr
420 425 430

Ala Arg Gln Ala Trp Glu Ala Cys Phe Asp Ser Tyr Met Gln Glu Ala
435 440 445

Lys Trp Ile Ala Thr Gly Tyr Leu Pro Thr Phe Glu Glu Tyr Leu Glu
450 455 460

Asn Gly Lys Val Ser Ser Ala His Arg Pro Cys Ala Leu Gln Pro Ile
465 470 475 480

Leu Thr Leu Asp Ile Pro Phe Pro Asp His Ile Leu Lys Glu Val Asp
485 490 495

Phe Pro Ser Lys Leu Asn Asp Leu Ile Cys Ile Ile Leu Arg Leu Arg
500 505 510

Gly Asp Thr Arg Cys Tyr Lys Ala Asp Arg Ala Arg Gly Glu Glu Ala
515 520 525

Ser Ser Ile Ser Cys Tyr Met Lys Asp Asn Pro Gly Leu Thr Glu Glu
530 535 540

Asp Ala Leu Asn His Ile Asn Phe Met Ile Arg Asp Ala Ile Arg Glu
545 550 555 560

Leu Asn Trp Glu Leu Leu Lys Pro Asp Asn Ser Val Pro Ile Thr Ser
565 570 575

Lys Lys His Ala Phe Asp Ile Ser Arg Val Trp His His Gly Tyr Arg
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Tyr Arg Asp Gly Tyr Ser Phe Ala Asn Val Glu Thr Lys Ser Leu Val

595

600

605

Met Arg Thr Val Ile Glu Pro Val Pro Leu
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Pro Lys Ser Cys Leu His Lys Ser Leu Ile Arg Ser Thr His His Glu
10 15 20

ctc aag cct ctg cgc aga acc atc cca act ctt gga atg tgt agg cga 150
Leu Lys Pro Leu Arg Arg Thr Ile Pro Thr Leu Gly Met Cys Arg Arg
25 30 35

ggg aaa tct ttc aca cct tct gtg agc atg agt ttg acc acc gct gta 198
Gly Lys Ser Phe Thr Pro Ser Val Ser Met Ser Leu Thr Thr Ala Val
40 45 50 55

tct gat gat ggt cta caa aga cgc ata ggt gac tat cat tcc aat ctc 246
Ser Asp Asp Gly Leu Gln Arg Arg Ile Gly Asp Tyr His Ser Asn Leu
60 65 70

tgg gac gac gat ttc ata cag tct cta tca acg cct tat ggg gag cct 294
Trp Asp Asp Asp Phe Ile Gln Ser Leu Ser Thr Pro Tyr Gly Glu Pro
75 80 85

tct tac cga gaa cgt gct gag aaa ctg att ggg gaa gtg aag gag atg 342
Ser Tyr Arg Glu Arg Ala Glu Lys Leu Ile Gly Glu Val Lys Glu Met
90 95 100

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Phe Asn Ser Met Pro Ser Glu Asp Gly Glu Ser Met Ser Pro Leu Asn
105 110 115

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Asp Leu Ile Glu Arg Leu Trp Met Val Asp Ser Val Glu Arg Leu Gly
120 125 130 135

att gat aga cat ttc aaa aaa gag ata aaa tca gcc ctt gat tat gtt 486
Ile Asp Arg His Phe Lys Lys Glu Ile Lys Ser Ala Leu Asp Tyr Val
140 145 150

tac agt tat tgg aac gaa aaa ggt att gga tgc ggt aga gat agt gtt 534
Tyr Ser Tyr Trp Asn Glu Lys Gly Ile Gly Cys Gly Arg Asp Ser Val

155	160	165	
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cac gga tac agt gtc tct tca gag gtt ttg aaa gta ttt caa gac caa His Gly Tyr Ser Val Ser Ser Glu Val Leu Lys Val Phe Gln Asp Gln 185 190 195			630
aat ggg cag ttt gca ttc tct cct agt aca aaa gag aga gac atc aga Asn Gly Gln Phe Ala Phe Ser Pro Ser Thr Lys Glu Arg Asp Ile Arg 200 205 210 215			678
acc gtt ctg aat tta tat cgg gct tct ttc att gcc ttt cct ggg gag Thr Val Leu Asn Leu Tyr Arg Ala Ser Phe Ile Ala Phe Pro Gly Glu 220 225 230			726
aaa gtt atg gaa gag gct gaa att ttc tct tca aga tat ttg aaa gaa Lys Val Met Glu Glu Ala Glu Ile Phe Ser Ser Arg Tyr Leu Lys Glu 235 240 245			774
gcc gtg caa aag att ccg gtc tcc agt ctt tca caa gaa ata gac tac Ala Val Gln Lys Ile Pro Val Ser Ser Leu Ser Gln Glu Ile Asp Tyr 250 255 260			822
act ttg gaa tat ggt tgg cac aca aat atg cca aga ttg gaa aca agg Thr Leu Glu Tyr Gly Trp His Thr Asn Met Pro Arg Leu Glu Thr Arg 265 270 275			870
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cgg cat cgt cac gtg gaa tac tac acc ctg agc tct tgc att gcg act Arg His Arg His Val Glu Tyr Tyr Thr Leu Ser Ser Cys Ile Ala Thr 345 350 355			1110
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gaa gcc tta act gac atg gcg cga gag gca gag aag aca caa ggc cga Glu Ala Leu Thr Asp Met Ala Arg Glu Ala Glu Lys Thr Gln Gly Arg 425 430 435	1350
gac acg ctc aat tat gct aga aag gct tgg gaa gtt tat ctt gat tcg Asp Thr Leu Asn Tyr Ala Arg Lys Ala Trp Glu Val Tyr Leu Asp Ser 440 445 450 455	1398
tat aca caa gaa gca aag tgg atc gcc agc ggt tat ctg cca act ttc Tyr Thr Gln Glu Ala Lys Trp Ile Ala Ser Gly Tyr Leu Pro Thr Phe 460 465 470	1446
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gga tta aca gag gaa gat gct ctc aat cat atc aat gcc atg atc aac Gly Leu Thr Glu Glu Asp Ala Leu Asn His Ile Asn Ala Met Ile Asn 555 560 565	1734
gac ata atc aaa gaa tta aat tgg gaa ctt ctc aaa ccc gat agc aat Asp Ile Ile Lys Glu Leu Asn Trp Glu Leu Leu Lys Pro Asp Ser Asn 570 575 580	1782
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cac caa ctt tac aaa tat aga gat ggc ttc agc gtt gcc act caa gaa His Gln Leu Tyr Lys Tyr Arg Asp Gly Phe Ser Val Ala Thr Gln Glu 600 605 610 615	1878
acg aaa agt ttg gtg agg aga acg gtc ctt gaa cca gtg cct ctt Thr Lys Ser Leu Val Arg Arg Thr Val Leu Glu Pro Val Pro Leu 620 625 630	1923
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